STIC-Biotech/ChemLib 119643

From: Hamud, Fozia
Sent: Sunday, April 18, 2004 8:10 AM
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Subject: sequence search for 09/989725

Kindly search SEQ ID NO:417 of 09/989725 against commercial and interference data bases. Thanks.

Fozia Hamud
Patent Examiner
Art Unit 1647
Remsen: Room 4D64
Mail Box Remsen: 4C70
272-0884

Searcher:_____
Phone:_____
Location:_____
Date Picked Up: 4/20/04
Date Completed: 4/20/04
Searcher Prep/Review:_____
Clerical:_____
Online time:_____

TYPE OF SEARCH: 1
NA Sequences:_____
AA Sequences:_____
Structures:_____
Bibliographic:_____
Litigation:_____
Full text:_____
Patent Family:_____
Other:_____

VENDOR/COST (where applic.)
STN:_____
DIALOG:_____
Questel/Orbit:_____
DRLink:_____
Lexis/Nexis:_____
Sequence Sys.: 004
WWW/Internet:_____
Other (specify):_____

STIC Search Report
Biotech-Chem Library

STIC Database Tracking Number: 119643

TO: Fozia Hamud **Location: REM/4D64/4C70** **Art Unit: 1647** **Tuesday, April 20, 2004** **Case Serial Number: 09/989725**	**From: Edward Hart** **Location: Biotech-Chem Library** **REM-1A55** **Phone: 571-272-2512** **edward.hart@uspto.gov**

Search Notes

Examiner Hamud,

Here are the results of the search you requested.

Please feel free to contact me if you have any questions.

Edward Hart

GenCore version 5.1.6

OM nucleic - nucleic search, using sw model

Run on: April 20, 2004, 01:40:55 ; Search time 692 Seconds
(without alignments)
10608.217 Million cell updates/sec

Title: US-09-989-725-417
Perfect score: 1728
Sequence: 1 cagccgggtcccaagcctgt.....aataatttttgaaacatcaa 1728

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 3373863 seqs, 2124099041 residues

Total number of hits satisfying chosen parameters: 6747726

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : N_Geneseq_29Jan04:*
1: geneseqn1980s:*
2: geneseqn1990s:*
3: geneseqn2000s:*
4: geneseqn2001as:*
5: geneseqn2001bs:*
6: geneseqn2002s:*
7: geneseqn2003as:*
8: geneseqn2003bs:*
9: geneseqn2003cs:*
10: geneseqn2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	1728	100.0	1728	3	AAZ65108	Aaz65108 Membrane-
2	1728	100.0	1728	4	AAC91568	Aac91568 Human PRO
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6	1728	100.0	1728	7	ABX77979	Abx77979 Human PRO
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ALIGNMENTS

RESULT 1
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ID AAZ65108 standard; cDNA; 1728 BP.
XX
AC AAZ65108;
XX
DT 05-APR-2000 (first entry)
XX
DE Membrane-bound protein PRO1375 encoding cDNA.
XX
KW Membrane-bound polypeptide; PRO polypeptide; LDL receptor; TIE ligand;
KW pharmaceutical; receptor immunoadhesin; gene mapping; ss.
XX
OS Homo sapiens.
XX
PN WO9963088-A2.
XX
PD 09-DEC-1999.
XX
PF 02-JUN-1999; 99WO-US012252.
XX
PR 02-JUN-1998; 98US-0087607P.
PR 02-JUN-1998; 98US-0087609P.
PR 02-JUN-1998; 98US-0087759P.
PR 03-JUN-1998; 98US-0087827P.
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PR 26-AUG-1998; 98US-0098014P.
PR 31-AUG-1998; 98US-0098525P.
PR 16-SEP-1998; 98US-0100634P.
PR 12-JAN-1999; 99US-0115565P.
XX
PA (GETH) GENENTECH INC.
XX
PI Baker K, Chen J, Goddard A, Gurney AL, Smith V, Watanabe CK;
PI Wood WI, Yuan J;
XX
DR WPI; 2000-072883/06.
DR P-PSDB; AAY66762.
XX
PT Membrane-bound proteins and related nucleotide sequences.
XX
PS Claim 2; Fig 299; 822pp; English.
XX
CC The invention provides membrane-bound PRO polypeptides and
CC polynucleotides encoding them. The PRO sequences of the invention were
CC identified based on extracellular domain homology screening. The PRO
CC sequences have homology with proteins including LDL receptors, TIE
CC ligands and various enzymes. The membrane-bound proteins and receptor
CC molecules are useful as pharmaceutical and diagnostic agents. Receptor
CC immunoadhesins, for instance, can be used as therapeutic agents to block
CC receptor-ligand interactions. The membrane-bound proteins can also be
CC employed for screening of potential peptide or small molecule inhibitors
CC of the relevant receptor/ligand interaction. The PRO encoding sequences
CC are useful as hybridization probes, in chromosome and gene mapping and in
CC the generation of antisense RNA and DNA. PRO nucleic acid sequences will
CC also be useful for the preparation of PRO polypeptides, especially by
CC recombinant techniques
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SQ Sequence 1728 BP; 438 A; 360 C; 390 G; 540 T; 0 U; 0 Other;

Query Match 100.0%; Score 1728; DB 3; Length 1728;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1728; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CAGCCGGGTCCCAAGCCTGTGCCTGAGCCTGAGCCTGAGCCTGAGCCCGAGCCGGGAGCC 60

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Db        121 AGGCCTTCTTCGGCTTGGCTCCTTGCTCAGCCTGTCGTGCCTGGCGCTTTCCGTGCTGCT 180
Qy        181 GCTGGCGCAGCTGTCAGACGCCGCCAAGAATTTCGAGGATGTCAGATGTAAATGTATCTG 240
Db        181 GCTGGCGCAGCTGTCAGACGCCGCCAAGAATTTCGAGGATGTCAGATGTAAATGTATCTG 240
Qy        241 CCCTCCCTATAAAGAAAATTCTGGGCATATTTATAATAAGAACATATCTCAGAAAGATTG 300
Db        241 CCCTCCCTATAAAGAAAATTCTGGGCATATTTATAATAAGAACATATCTCAGAAAGATTG 300
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RESULT 2
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ID   AAC91568 standard; cDNA; 1728 BP.
XX
AC   AAC91568;
XX
DT   21-MAR-2001  (first entry)
XX
DE   Human PRO1375 cDNA.
XX
KW   Human; PRO; cytostatic; nootropic; neuroprotective; respiratory general;
KW   antiinflammatory; antiangiogenic; immunosuppressive; immunostimulant;
KW   PRO agonist; cancer; inflammatory disorder; immunological disorder; ss.
XX
OS   Homo sapiens.
XX
PN   WO200073348-A2.
XX
PD   07-DEC-2000.
XX
PF   30-MAY-2000; 2000WO-US014941.
XX
PR   02-JUN-1999;   99WO-US012252.
PR   22-JUN-1999;   99US-0140650P.
PR   23-JUN-1999;   99US-0141037P.
PR   20-JUL-1999;   99US-0144758P.
PR   01-SEP-1999;   99WO-US020111.
PR   08-SEP-1999;   99WO-US020594.
PR   29-OCT-1999;   99US-0162506P.
PR   30-NOV-1999;   99WO-US028313.
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PR 01-DEC-1999; 99WO-US028634.
PR 02-DEC-1999; 99WO-US028551.
PR 09-DEC-1999; 99US-0170262P.
PR 16-DEC-1999; 99WO-US030095.
PR 20-DEC-1999; 99WO-US030999.
PR 06-JAN-2000; 2000WO-US000376.
PR 11-FEB-2000; 2000WO-US003565.
PR 18-FEB-2000; 2000WO-US004341.
PR 18-FEB-2000; 2000WO-US004342.
PR 02-MAR-2000; 2000WO-US005841.
PR 03-MAR-2000; 2000US-0187202P.
PR 10-MAR-2000; 2000WO-US006319.
PR 15-MAR-2000; 2000WO-US006884.
PR 30-MAR-2000; 2000WO-US008439.
PR 17-MAY-2000; 2000WO-US013705.
XX
PA (GETH) GENENTECH INC.
XX
PI Baker KP, Goddard A, Gurney AL, Hebert C, Henzel W, Kabakoff RC;
PI Shelton DL, Smith V, Watanabe CK, Wood WI;
XX
DR WPI; 2001-016509/02.
DR P-PSDB; AAB50966.
XX
PT Twenty eight nucleic acids encoding PRO polypeptides which are useful for
PT treating various tumors, e.g. breast cancer, and other inflammatory,
PT angiogenic and immunological disorders.
XX
PS Claim 20; Fig 31; 188pp; English.
XX
CC The present sequence is one of twenty eight nucleic acids encoding PRO
CC polypeptides. The PRO polypeptides and their agonists, including
CC antibodies, peptides, and small molecule agonists, may be used to treat
CC various tumours, e.g., cancers such as breast cancer, ovarian cancer,
CC renal cancer, colorectal cancer, uterine cancer, prostate cancer, lung
CC cancer, bladder cancer, central nervous system cancer, melanoma or
CC leukaemia. They are also useful for treating other disorders such as
CC neuronal, glial, astrocytal, hypothalamic and other glandular,
CC macrophagal, epithelial, stromal and blastocoelic disorders, and
CC inflammatory, angiogenic and immunological disorders
XX
SQ Sequence 1728 BP; 438 A; 360 C; 390 G; 540 T; 0 U; 0 Other;

Query Match 100.0%; Score 1728; DB 4; Length 1728;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1728; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy          1 CAGCCGGGTCCCAAGCCTGTGCCTGAGCCTGAGCCTGAGCCTGAGCCCGAGCCGGGAGCC 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 CAGCCGGGTCCCAAGCCTGTGCCTGAGCCTGAGCCTGAGCCTGAGCCCGAGCCGGGAGCC 60

Qy         61 GGTCGCGGGGGGCTCCGGGCTGTGGGACCGCTGGGCCCCCCAGCGATGGCGACCCTGTGGGG 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 GGTCGCGGGGGGCTCCGGGCTGTGGGACCGCTGGGCCCCCCAGCGATGGCGACCCTGTGGGG 120

Qy        121 AGGCCTTCTTCGGCTTGGCTCCTTGCTCAGCCTGTCGTGCCTGGCGCTTTCCGTGCTGCT 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 AGGCCTTCTTCGGCTTGGCTCCTTGCTCAGCCTGTCGTGCCTGGCGCTTTCCGTGCTGCT 180

Qy        181 GCTGGCGCAGCTGTCAGACGCCGCCAAGAATTTCGAGGATGTCAGATGTAAATGTATCTG 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 GCTGGCGCAGCTGTCAGACGCCGCCAAGAATTTCGAGGATGTCAGATGTAAATGTATCTG 240

Qy        241 CCCTCCCTATAAAGAAAATTCTGGGCATATTTATAATAAGAACATATCTCAGAAAGATTG 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 CCCTCCCTATAAAGAAAATTCTGGGCATATTTATAATAAGAACATATCTCAGAAAGATTG 300

Qy        301 TGATTGCCTTCATGTTGTGGAGCCCATGCCTGTGCGGGGGCCTGATGTAGAAGCATACTG 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 TGATTGCCTTCATGTTGTGGAGCCCATGCCTGTGCGGGGGCCTGATGTAGAAGCATACTG 360

Qy        361 TCTACGCTGTGAATGCAAATATGAAGAAAGAAGCTCTGTCACAATCAAGGTTACCATTAT 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 TCTACGCTGTGAATGCAAATATGAAGAAAGAAGCTCTGTCACAATCAAGGTTACCATTAT 420

Qy        421 AATTTATCTCTCCATTTTGGGCCTTCTACTTCTGTACATGGTATATCTTACTCTGGTTGA 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        421 AATTTATCTCTCCATTTTGGGCCTTCTACTTCTGTACATGGTATATCTTACTCTGGTTGA 480

Qy        481 GCCCATACTGAAGAGGCGCCTCTTTGGACATGCACAGTTGATACAGAGTGATGATGATAT 540
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        481 GCCCATACTGAAGAGGCGCCTCTTTGGACATGCACAGTTGATACAGAGTGATGATGATAT 540

Qy        541 TGGGGATCACCAGCCTTTTGCAAATGCACACGATGTGCTAGCCCGCTCCCGCAGTCGAGC 600
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        541 TGGGGATCACCAGCCTTTTGCAAATGCACACGATGTGCTAGCCCGCTCCCGCAGTCGAGC 600

Qy        601 CAACGTGCTGAACAAGGTAGAATATGCACAGCAGCGCTGGAAGCTTCAAGTCCAAGAGCA 660
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        601 CAACGTGCTGAACAAGGTAGAATATGCACAGCAGCGCTGGAAGCTTCAAGTCCAAGAGCA 660

Qy        661 GCGAAAGTCTGTCTTTGACCGGCATGTTGTCCTCAGCTAATTGGGAATTGAATTCAAGGT 720
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        661 GCGAAAGTCTGTCTTTGACCGGCATGTTGTCCTCAGCTAATTGGGAATTGAATTCAAGGT 720

Qy        721 GACTAGAAAGAAACAGGCAGACAACTGGAAAGAACTGACTGGGTTTTGCTGGGTTTCATT 780
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        721 GACTAGAAAGAAACAGGCAGACAACTGGAAAGAACTGACTGGGTTTTGCTGGGTTTCATT 780

Qy        781 TTAATACCTTGTTGATTTCACCAACTGTTGCTGGAAGATTCAAAACTGGAAGCAAAAACT 840
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        781 TTAATACCTTGTTGATTTCACCAACTGTTGCTGGAAGATTCAAAACTGGAAGCAAAAACT 840

Qy        841 TGCTTGATTTTTTTTTCTTGTTAACGTAATAATAGAGACATTTTTAAAAGCACACAGCTC 900
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        841 TGCTTGATTTTTTTTTCTTGTTAACGTAATAATAGAGACATTTTTAAAAGCACACAGCTC 900

Qy        901 AAAGTCAGCCAATAAGTCTTTTCCTATTTGTGACTTTTACTAATAAAAATAAATCTGCCT 960
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        901 AAAGTCAGCCAATAAGTCTTTTCCTATTTGTGACTTTTACTAATAAAAATAAATCTGCCT 960

Qy        961 GTAAATTATCTTGAAGTCCTTTACCTGGAACAAGCACTCTCTTTTTCACCACATAGTTTT 1020
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        961 GTAAATTATCTTGAAGTCCTTTACCTGGAACAAGCACTCTCTTTTTCACCACATAGTTTT 1020

Qy       1021 AACTTGACTTTCAAGATAATTTTCAGGGTTTTTGTTGTTGTTGTTTTTTGTTTGTTTGTT 1080
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1021 AACTTGACTTTCAAGATAATTTTCAGGGTTTTTGTTGTTGTTGTTTTTTGTTTGTTTGTT 1080

Qy       1081 TTGGTGGGAGAGGGGAGGGATGCCTGGGAAGTGGTTAACAACTTTTTTCAAGTCACTTTA 1140
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1081 TTGGTGGGAGAGGGGAGGGATGCCTGGGAAGTGGTTAACAACTTTTTTCAAGTCACTTTA 1140

Qy       1141 CTAAACAAACTTTTGTAAATAGACCTTACCTTCTATTTTCGAGTTTCATTTATATTTTGC 1200
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1141 CTAAACAAACTTTTGTAAATAGACCTTACCTTCTATTTTCGAGTTTCATTTATATTTTGC 1200

Qy       1201 AGTGTAGCCAGCCTCATCAAAGAGCTGACTTACTCATTTGACTTTTGCACTGACTGTATT 1260
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1201 AGTGTAGCCAGCCTCATCAAAGAGCTGACTTACTCATTTGACTTTTGCACTGACTGTATT 1260

Qy       1261 ATCTGGGTATCTGCTGTGTCTGCACTTCATGGTAAACGGGATCTAAAATGCCTGGTGGCT 1320
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1261 ATCTGGGTATCTGCTGTGTCTGCACTTCATGGTAAACGGGATCTAAAATGCCTGGTGGCT 1320

Qy       1321 TTTCACAAAAAGCAGATTTTCTTCATGTACTGTGATGTCTGATGCAATGCATCCTAGAAC 1380
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1321 TTTCACAAAAAGCAGATTTTCTTCATGTACTGTGATGTCTGATGCAATGCATCCTAGAAC 1380

Qy       1381 AAACTGGCCATTTGCTAGTTTACTCTAAAGACTAAACATAGTCTTGGTGTGTGTGGTCTT 1440
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1381 AAACTGGCCATTTGCTAGTTTACTCTAAAGACTAAACATAGTCTTGGTGTGTGTGGTCTT 1440

Qy       1441 ACTCATCTTCTAGTACCTTTAAGGACAAATCCTAAGGACTTGGACACTTGCAATAAAGAA 1500
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1441 ACTCATCTTCTAGTACCTTTAAGGACAAATCCTAAGGACTTGGACACTTGCAATAAAGAA 1500
```

```
Qy       1501 ATTTTATTTTAAACCCAAGCCTCCCTGGATTGATAATATATACACATTTGTCAGCATTTC 1560
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1501 ATTTTATTTTAAACCCAAGCCTCCCTGGATTGATAATATATACACATTTGTCAGCATTTC 1560

Qy       1561 CGGTCGTGGTGAGAGGCAGCTGTTTGAGCTCCAATATGTGCAGCTTTGAACTAGGGCTGG 1620
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1561 CGGTCGTGGTGAGAGGCAGCTGTTTGAGCTCCAATATGTGCAGCTTTGAACTAGGGCTGG 1620

Qy       1621 GGTTGTGGGTGCCTCTTCTGAAAGGTCTAACCATTATTGGATAACTGGCTTTTTTCTTCC 1680
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1621 GGTTGTGGGTGCCTCTTCTGAAAGGTCTAACCATTATTGGATAACTGGCTTTTTTCTTCC 1680

Qy       1681 TATGTCCTCTTTGGAATGTAACAATAAAAATAATTTTTGAAACATCAA 1728
             ||||||||||||||||||||||||||||||||||||||||||||||||
Db       1681 TATGTCCTCTTTGGAATGTAACAATAAAAATAATTTTTGAAACATCAA 1728
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RESULT 3
AAF30062
ID AAF30062 standard; cDNA; 1728 BP.
XX
AC AAF30062;
XX
DT 30-APR-2001 (first entry)
XX
DE Human cDNA encoding PRO1375.
XX
KW PRO1375; UNQ712; human; immune disease; autoimmune disease;
KW antirheumatic; antiarthritic; antiinflammatory; antianaemic;
KW immunosuppressive; antithyroid; antidiabetic; neuroprotective;
KW hepatotropic; virucide; dermatological; antipsoriatic; antiasthmatic;
KW antiallergic; immunostimulant; ss.
XX
OS Homo sapiens.
XX
FH Key Location/Qualifiers
FT CDS 104. .700
FT /*tag= a
XX
PN WO200105972-A1.
XX
PD 25-JAN-2001.
XX
PF 15-MAR-2000; 2000WO-US006884.
XX
PR 20-JUL-1999; 99US-0144758P.
XX
PA (GETH) GENENTECH INC.
XX
PI Ashkenazi AJ, Baker KP, Fong S, Goddard A, Godowski PJ;
PI Gurney AL, Hillan KJ, Mark MR, Marsters SA, Pitti RM, Tumas D;
PI Watanabe CK, Wood WI;
XX
DR WPI; 2001-103149/11.
DR P-PSDB; AAB20120.
XX
PT New PRO polypeptides, nucleic acids and (ant)agonists, useful for
PT diagnosing and treating immune-related disorders, such as multiple
PT sclerosis, rheumatoid arthritis and diabetes.
XX
PS Claim 21; Fig 25; 127pp; English.
XX
CC The present sequence is that of cDNA clone DNA67004-1614 (ATCC 203115)
CC encoding novel human immunomodulator protein PRO1375 (UNQ712) (see
CC AAB20120). The clone was isolated from a pancreas cDNA library. PRO1375
CC has a mol.wt. of 22 kDa and a pI of 8.47. The invention provides
CC polynucleotides (see AAF30050-62) encoding novel human PRO proteins (see
CC AAB20108-20) including PRO1375. Claimed compositions comprising these
CC proteins or their agonists are useful for increasing infiltration of
CC inflammatory cells into a tissue of a mammal, stimulating or enhancing an
CC immune response in a mammal, or increasing the proliferation of T-
CC lymphocytes in a mammal in response to an antigen. Claimed compositions
CC comprising the PRO polypeptide or its antagonist have the opposite
CC effect. A claimed method for treating an immune related disorder, such as
CC a T cell disorder, involves administering the PRO polypeptide, an agonist
CC antibody or an antagonist antibody. The disorder is selected from
CC systemic lupus erythematosus, rheumatoid arthritis, osteoarthritis,
CC juvenile chronic arthritis, spondyloarthropathy, systemic sclerosis,
CC idiopathic inflammatory myopathy, Sjogren's syndrome, systemic
CC vasculitis, sarcoidosis, autoimmune haemolytic anaemia, autoimmune
CC thrombocytopaenia, thyroiditis, diabetes mellitus, immune-mediated renal
CC disease, demyelinated diseases (such as multiple sclerosis), autoimmune
CC chronic active hepatitis, primary biliary cirrhosis, granulomatous
CC hepatitis, sclerosing cholangitis, inflammatory bowel disease (ulcerative
CC colitis and Crohn's disease), gluten-sensitive enteropathy, Whipple's
CC disease, (auto)immune-mediated skin diseases (such as bullous skin
CC disease, erythema multiforme and psoriasis), allergic diseases (such as
CC asthma, allergic rhinitis, atopic dermatitis, food hypersensitivity and
CC urticaria), immunologic diseases of the lung and transplantation
CC associated diseases (such as graft rejection and graft-versus-host
CC disease) (all claimed). Claimed methods of diagnosing these disorders
CC comprise detecting the level of expression of the PRO gene. Also claimed
CC are a method of identifying a compound capable of inhibiting the
CC expression or activity of the PRO polypeptide, vectors, host cells,
CC antibodies and a method of stimulating the proliferation of T-lymphocytes
CC using PRO1375
XX
SQ Sequence 1728 BP; 438 A; 360 C; 390 G; 540 T; 0 U; 0 Other;

Query Match 100.0%; Score 1728; DB 4; Length 1728;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1728; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy          1 CAGCCGGGTCCCAAGCCTGTGCCTGAGCCTGAGCCTGAGCCTGAGCCCGAGCCGGGAGCC 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 CAGCCGGGTCCCAAGCCTGTGCCTGAGCCTGAGCCTGAGCCTGAGCCCGAGCCGGGAGCC 60

Qy         61 GGTCGCGGGGGGCTCCGGGCTGTGGGACCGCTGGGCCCCCAGCGATGGCGACCCTGTGGGG 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 GGTCGCGGGGGGCTCCGGGCTGTGGGACCGCTGGGCCCCCAGCGATGGCGACCCTGTGGGG 120

Qy        121 AGGCCTTCTTCGGCTTGGCTCCTTGCTCAGCCTGTCGTGCCTGGCGCTTTCCGTGCTGCT 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 AGGCCTTCTTCGGCTTGGCTCCTTGCTCAGCCTGTCGTGCCTGGCGCTTTCCGTGCTGCT 180

Qy        181 GCTGGCGCAGCTGTCAGACGCCGCCAAGAATTTCGAGGATGTCAGATGTAAATGTATCTG 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 GCTGGCGCAGCTGTCAGACGCCGCCAAGAATTTCGAGGATGTCAGATGTAAATGTATCTG 240

Qy        241 CCCTCCCTATAAAGAAAATTCTGGGCATATTTATAATAAGAACATATCTCAGAAAGATTG 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 CCCTCCCTATAAAGAAAATTCTGGGCATATTTATAATAAGAACATATCTCAGAAAGATTG 300

Qy        301 TGATTGCCTTCATGTTGTGGAGCCCATGCCTGTGCGGGGGCCTGATGTAGAAGCATACTG 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 TGATTGCCTTCATGTTGTGGAGCCCATGCCTGTGCGGGGGCCTGATGTAGAAGCATACTG 360

Qy        361 TCTACGCTGTGAATGCAAATATGAAGAAAGAAGCTCTGTCACAATCAAGGTTACCATTAT 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 TCTACGCTGTGAATGCAAATATGAAGAAAGAAGCTCTGTCACAATCAAGGTTACCATTAT 420

Qy        421 AATTTATCTCTCCATTTTGGGCCTTCTACTTCTGTACATGGTATATCTTACTCTGGTTGA 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        421 AATTTATCTCTCCATTTTGGGCCTTCTACTTCTGTACATGGTATATCTTACTCTGGTTGA 480

Qy        481 GCCCATACTGAAGAGGCGCCTCTTTGGACATGCACAGTTGATACAGAGTGATGATGATAT 540
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        481 GCCCATACTGAAGAGGCGCCTCTTTGGACATGCACAGTTGATACAGAGTGATGATGATAT 540

Qy        541 TGGGGATCACCAGCCTTTTGCAAATGCACACGATGTGCTAGCCCGCTCCCGCAGTCGAGC 600
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        541 TGGGGATCACCAGCCTTTTGCAAATGCACACGATGTGCTAGCCCGCTCCCGCAGTCGAGC 600

Qy        601 CAACGTGCTGAACAAGGTAGAATATGCACAGCAGCGCTGGAAGCTTCAAGTCCAAGAGCA 660
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Db        601 CAACGTGCTGAACAAGGTAGAATATGCACAGCAGCGCTGGAAGCTTCAAGTCCAAGAGCA 660

Qy        661 GCGAAAGTCTGTCTTTGACCGGCATGTTGTCCTCAGCTAATTGGGAATTGAATTCAAGGT 720
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        661 GCGAAAGTCTGTCTTTGACCGGCATGTTGTCCTCAGCTAATTGGGAATTGAATTCAAGGT 720

Qy        721 GACTAGAAAGAAACAGGCAGACAACTGGAAAGAACTGACTGGGTTTTGCTGGGTTTCATT 780
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        721 GACTAGAAAGAAACAGGCAGACAACTGGAAAGAACTGACTGGGTTTTGCTGGGTTTCATT 780

Qy        781 TTAATACCTTGTTGATTTCACCAACTGTTGCTGGAAGATTCAAAACTGGAAGCAAAAACT 840
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        781 TTAATACCTTGTTGATTTCACCAACTGTTGCTGGAAGATTCAAAACTGGAAGCAAAAACT 840

Qy        841 TGCTTGATTTTTTTTTCTTGTTAACGTAATAATAGAGACATTTTTAAAAGCACACAGCTC 900
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        841 TGCTTGATTTTTTTTTCTTGTTAACGTAATAATAGAGACATTTTTAAAAGCACACAGCTC 900

Qy        901 AAAGTCAGCCAATAAGTCTTTTCCTATTTGTGACTTTTACTAATAAAAATAAATCTGCCT 960
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        901 AAAGTCAGCCAATAAGTCTTTTCCTATTTGTGACTTTTACTAATAAAAATAAATCTGCCT 960

Qy        961 GTAAATTATCTTGAAGTCCTTTACCTGGAACAAGCACTCTCTTTTTCACCACATAGTTTT 1020
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        961 GTAAATTATCTTGAAGTCCTTTACCTGGAACAAGCACTCTCTTTTTCACCACATAGTTTT 1020

Qy       1021 AACTTGACTTTCAAGATAATTTTCAGGGTTTTTGTTGTTGTTGTTTTTTGTTTGTTTGTT 1080
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1021 AACTTGACTTTCAAGATAATTTTCAGGGTTTTTGTTGTTGTTGTTTTTTGTTTGTTTGTT 1080

Qy       1081 TTGGTGGGAGAGGGGAGGGATGCCTGGGAAGTGGTTAACAACTTTTTTCAAGTCACTTTA 1140
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1081 TTGGTGGGAGAGGGGAGGGATGCCTGGGAAGTGGTTAACAACTTTTTTCAAGTCACTTTA 1140

Qy       1141 CTAAACAAACTTTTGTAAATAGACCTTACCTTCTATTTTCGAGTTTCATTTATATTTTGC 1200
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1141 CTAAACAAACTTTTGTAAATAGACCTTACCTTCTATTTTCGAGTTTCATTTATATTTTGC 1200

Qy       1201 AGTGTAGCCAGCCTCATCAAAGAGCTGACTTACTCATTTGACTTTTGCACTGACTGTATT 1260
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1201 AGTGTAGCCAGCCTCATCAAAGAGCTGACTTACTCATTTGACTTTTGCACTGACTGTATT 1260

Qy       1261 ATCTGGGTATCTGCTGTGTCTGCACTTCATGGTAAACGGGATCTAAAATGCCTGGTGGCT 1320
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1261 ATCTGGGTATCTGCTGTGTCTGCACTTCATGGTAAACGGGATCTAAAATGCCTGGTGGCT 1320

Qy       1321 TTTCACAAAAAGCAGATTTTCTTCATGTACTGTGATGTCTGATGCAATGCATCCTAGAAC 1380
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1321 TTTCACAAAAAGCAGATTTTCTTCATGTACTGTGATGTCTGATGCAATGCATCCTAGAAC 1380

Qy       1381 AAACTGGCCATTTGCTAGTTTACTCTAAAGACTAAACATAGTCTTGGTGTGTGTGGTCTT 1440
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1381 AAACTGGCCATTTGCTAGTTTACTCTAAAGACTAAACATAGTCTTGGTGTGTGTGGTCTT 1440

Qy       1441 ACTCATCTTCTAGTACCTTTAAGGACAAATCCTAAGGACTTGGACACTTGCAATAAAGAA 1500
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1441 ACTCATCTTCTAGTACCTTTAAGGACAAATCCTAAGGACTTGGACACTTGCAATAAAGAA 1500

Qy       1501 ATTTTATTTTAAACCCAAGCCTCCCTGGATTGATAATATATACACATTTGTCAGCATTTC 1560
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1501 ATTTTATTTTAAACCCAAGCCTCCCTGGATTGATAATATATACACATTTGTCAGCATTTC 1560

Qy       1561 CGGTCGTGGTGAGAGGCAGCTGTTTGAGCTCCAATATGTGCAGCTTTGAACTAGGGCTGG 1620
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1561 CGGTCGTGGTGAGAGGCAGCTGTTTGAGCTCCAATATGTGCAGCTTTGAACTAGGGCTGG 1620

Qy       1621 GGTTGTGGGTGCCTCTTCTGAAAGGTCTAACCATTATTGGATAACTGGCTTTTTTCTTCC 1680
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1621 GGTTGTGGGTGCCTCTTCTGAAAGGTCTAACCATTATTGGATAACTGGCTTTTTTCTTCC 1680

Qy       1681 TATGTCCTCTTTGGAATGTAACAATAAAAATAATTTTTGAAACATCAA 1728
              ||||||||||||||||||||||||||||||||||||||||||||||||
Db       1681 TATGTCCTCTTTGGAATGTAACAATAAAAATAATTTTTGAAACATCAA 1728
```

RESULT 4
AAC91485
ID AAC91485 standard; cDNA; 1728 BP.
XX
AC AAC91485;
XX
DT 21-MAR-2001 (first entry)
XX
DE Human PRO1375 cDNA.
XX
KW Human; PRO; antiinflammatory; dermatological; antiarthritic;
KW antirheumatic; cardiant; antianaemic; immunosuppressive; antithyroid;
KW antidiabetic; nootropic; neuroprotective; hepatotropic; virucide;
KW antiallergic; antiasthmatic; immune related disorder;
KW hepatobiliary disease; autoimmune disease; allergy; ss.
XX
OS Homo sapiens.
XX
PN WO200073452-A2.
XX
PD 07-DEC-2000.
XX
PF 02-JUN-2000; 2000WO-US015264.
XX
PR 02-JUN-1999; 99WO-US012252.
PR 20-JUL-1999; 99US-0144732P.
PR 20-JUL-1999; 99US-0144758P.
PR 28-JUL-1999; 99US-0146222P.
PR 01-SEP-1999; 99WO-US020111.
PR 15-SEP-1999; 99WO-US021090.
PR 15-SEP-1999; 99WO-US021547.
PR 29-OCT-1999; 99US-0162506P.
PR 30-NOV-1999; 99WO-US028313.
PR 01-DEC-1999; 99WO-US028634.
PR 02-DEC-1999; 99WO-US028551.
PR 02-DEC-1999; 99WO-US028565.
PR 09-DEC-1999; 99US-0170262P.
PR 20-DEC-1999; 99WO-US030911.
PR 05-JAN-2000; 2000WO-US000219.
PR 06-JAN-2000; 2000WO-US000376.
PR 11-FEB-2000; 2000WO-US003565.
PR 18-FEB-2000; 2000WO-US004341.
PR 18-FEB-2000; 2000WO-US004342.
PR 22-FEB-2000; 2000WO-US004414.
PR 24-FEB-2000; 2000WO-US004914.
PR 24-FEB-2000; 2000WO-US005004.
PR 01-MAR-2000; 2000WO-US005601.
PR 02-MAR-2000; 2000WO-US005841.
PR 03-MAR-2000; 2000US-0187202P.
PR 15-MAR-2000; 2000WO-US006884.
PR 20-MAR-2000; 2000WO-US007377.
PR 21-MAR-2000; 2000WO-US007532.
PR 30-MAR-2000; 2000WO-US008439.
PR 17-MAY-2000; 2000WO-US013705.
PR 22-MAY-2000; 2000WO-US014042.
XX
PA (GETH) GENENTECH INC.
XX
PI Ashkenazi AJ, Baker KP, Chan B, Goddard A, Godowski PJ;
PI Gurney AL, Hebert C, Henzel W, Kabakoff RC, Shelton DL, Tumas D;
PI Watanabe CK, Wood WI;
XX
DR WPI; 2001-025253/03.
DR P-PSDB; AAB50926.
XX
PT Thirty three nucleic acids encoding PRO polypeptides which are useful in
PT the diagnosis and treatment of immune related disorders, e.g. systemic
PT lupus erythematosis, rheumatoid arthritis, osteoarthritis, thyroiditis
PT and diabetes mellitus.
XX
PS Claim 48; Fig 49; 218pp; English.

XX
CC The present sequence is one of thirty three nucleic acids encoding PRO
CC polypeptides. The PRO polypeptides, anti-PRO antibodies, agonists and
CC antagonists are useful for treating and diagnosing immune related
CC disorders such as systemic lupus erythematosus, rheumatoid arthritis,
CC osteoarthritis, juvenile chronic arthritis, spondyloarthropathies,
CC systemic sclerosis, idiopathic inflammatory myopathies, Sjogren's
CC syndrome, systemic vasculitis, sarcoidosis, autoimmune haemolytic
CC anaemia, autoimmune thrombocytopaenia, thyroiditis, diabetes mellitus,
CC immune-mediated renal disease, demyelinating diseases of the central and
CC peripheral nervous systems (such as multiple sclerosis, idiopathic
CC demyelinating polyneuropathy or Guillain-Barre syndrome, and chronic
CC inflammatory demyelinating polyneuropathy), hepatobiliary diseases (such
CC as infectious, autoimmune chronic active hepatitis, primary biliary
CC cirrhosis, granulomatous hepatitis and sclerosing cholangitis),
CC inflammatory bowel disease, gluten-sensitive enteropathy and Whipple's
CC disease, autoimmune or immune-mediated skin diseases (such as bullous
CC skin diseases, erythema multiforme, contact dermatitis, psoriasis),
CC allergic diseases such as asthma, allergic rhinitis, atopic dermatitis,
CC food hypersensitivity and urticaria), immunological diseases of the lung
CC (such as eosinophilic pneumonias, idiopathic pulmonary fibrosis and
CC hypersensitivity pneumonitis), transplantation associated diseases
CC including graft rejection and graft-versus-host diseases
XX
SQ Sequence 1728 BP; 438 A; 360 C; 390 G; 540 T; 0 U; 0 Other;

Query Match 100.0%; Score 1728; DB 5; Length 1728;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1728; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy    1 CAGCCGGGTCCCAAGCCTGTGCCTGAGCCTGAGCCTGAGCCTGAGCCCGAGCCGGGAGCC 60
Db    1 CAGCCGGGTCCCAAGCCTGTGCCTGAGCCTGAGCCTGAGCCTGAGCCCGAGCCGGGAGCC 60

Qy   61 GGTCGCGGGGGCTCCGGGCTGTGGGACCGCTGGGCCCCCAGCGATGGCGACCCTGTGGGG 120
Db   61 GGTCGCGGGGGCTCCGGGCTGTGGGACCGCTGGGCCCCCAGCGATGGCGACCCTGTGGGG 120

Qy  121 AGGCCTTCTTCGGCTTGGCTCCTTGCTCAGCCTGTCGTGCCTGGCGCTTTCCGTGCTGCT 180
Db  121 AGGCCTTCTTCGGCTTGGCTCCTTGCTCAGCCTGTCGTGCCTGGCGCTTTCCGTGCTGCT 180

Qy  181 GCTGGCGCAGCTGTCAGACGCCGCCAAGAATTTCGAGGATGTCAGATGTAAATGTATCTG 240
Db  181 GCTGGCGCAGCTGTCAGACGCCGCCAAGAATTTCGAGGATGTCAGATGTAAATGTATCTG 240

Qy  241 CCCTCCCTATAAAGAAAATTCTGGGCATATTTATAATAAGAACATATCTCAGAAAGATTG 300
Db  241 CCCTCCCTATAAAGAAAATTCTGGGCATATTTATAATAAGAACATATCTCAGAAAGATTG 300

Qy  301 TGATTGCCTTCATGTTGTGGAGCCCATGCCTGTGCGGGGGCCTGATGTAGAAGCATACTG 360
Db  301 TGATTGCCTTCATGTTGTGGAGCCCATGCCTGTGCGGGGGCCTGATGTAGAAGCATACTG 360

Qy  361 TCTACGCTGTGAATGCAAATATGAAGAAAGAAGCTCTGTCACAATCAAGGTTACCATTAT 420
Db  361 TCTACGCTGTGAATGCAAATATGAAGAAAGAAGCTCTGTCACAATCAAGGTTACCATTAT 420

Qy  421 AATTTATCTCTCCATTTTGGGCCTTCTACTTCTGTACATGGTATATCTTACTCTGGTTGA 480
Db  421 AATTTATCTCTCCATTTTGGGCCTTCTACTTCTGTACATGGTATATCTTACTCTGGTTGA 480

Qy  481 GCCCATACTGAAGAGGCGCCTCTTTGGACATGCACAGTTGATACAGAGTGATGATGATAT 540
Db  481 GCCCATACTGAAGAGGCGCCTCTTTGGACATGCACAGTTGATACAGAGTGATGATGATAT 540

Qy  541 TGGGGATCACCAGCCTTTTGCAAATGCACACGATGTGCTAGCCCGCTCCCGCAGTCGAGC 600
Db  541 TGGGGATCACCAGCCTTTTGCAAATGCACACGATGTGCTAGCCCGCTCCCGCAGTCGAGC 600

Qy  601 CAACGTGCTGAACAAGGTAGAATATGCACAGCAGCGCTGGAAGCTTCAAGTCCAAGAGCA 660
Db  601 CAACGTGCTGAACAAGGTAGAATATGCACAGCAGCGCTGGAAGCTTCAAGTCCAAGAGCA 660

Qy  661 GCGAAAGTCTGTCTTTGACCGGCATGTTGTCCTCAGCTAATTGGGAATTGAATTCAAGGT 720
Db  661 GCGAAAGTCTGTCTTTGACCGGCATGTTGTCCTCAGCTAATTGGGAATTGAATTCAAGGT 720

Qy  721 GACTAGAAAGAAACAGGCAGACAACTGGAAAGAACTGACTGGGTTTTGCTGGGTTTCATT 780
Db  721 GACTAGAAAGAAACAGGCAGACAACTGGAAAGAACTGACTGGGTTTTGCTGGGTTTCATT 780

Qy  781 TTAATACCTTGTTGATTTCACCAACTGTTGCTGGAAGATTCAAAACTGGAAGCAAAAACT 840
Db  781 TTAATACCTTGTTGATTTCACCAACTGTTGCTGGAAGATTCAAAACTGGAAGCAAAAACT 840

Qy  841 TGCTTGATTTTTTTTTCTTGTTAACGTAATAATAGAGACATTTTTAAAAGCACACAGCTC 900
Db  841 TGCTTGATTTTTTTTTCTTGTTAACGTAATAATAGAGACATTTTTAAAAGCACACAGCTC 900

Qy  901 AAAGTCAGCCAATAAGTCTTTTCCTATTTGTGACTTTTACTAATAAAAATAAATCTGCCT 960
Db  901 AAAGTCAGCCAATAAGTCTTTTCCTATTTGTGACTTTTACTAATAAAAATAAATCTGCCT 960

Qy  961 GTAAATTATCTTGAAGTCCTTTACCTGGAACAAGCACTCTCTTTTTCACCACATAGTTTT 1020
Db  961 GTAAATTATCTTGAAGTCCTTTACCTGGAACAAGCACTCTCTTTTTCACCACATAGTTTT 1020

Qy 1021 AACTTGACTTTCAAGATAATTTTCAGGGTTTTTGTTGTTGTTGTTTTTTGTTTGTTTGTT 1080
Db 1021 AACTTGACTTTCAAGATAATTTTCAGGGTTTTTGTTGTTGTTGTTTTTTGTTTGTTTGTT 1080

Qy 1081 TTGGTGGGAGAGGGGAGGGATGCCTGGGAAGTGGTTAACAACTTTTTTCAAGTCACTTTA 1140
Db 1081 TTGGTGGGAGAGGGGAGGGATGCCTGGGAAGTGGTTAACAACTTTTTTCAAGTCACTTTA 1140

Qy 1141 CTAAACAAACTTTTGTAAATAGACCTTACCTTCTATTTTCGAGTTTCATTTATATTTTGC 1200
Db 1141 CTAAACAAACTTTTGTAAATAGACCTTACCTTCTATTTTCGAGTTTCATTTATATTTTGC 1200

Qy 1201 AGTGTAGCCAGCCTCATCAAAGAGCTGACTTACTCATTTGACTTTTGCACTGACTGTATT 1260
Db 1201 AGTGTAGCCAGCCTCATCAAAGAGCTGACTTACTCATTTGACTTTTGCACTGACTGTATT 1260

Qy 1261 ATCTGGGTATCTGCTGTGTCTGCACTTCATGGTAAACGGGATCTAAAATGCCTGGTGGCT 1320
Db 1261 ATCTGGGTATCTGCTGTGTCTGCACTTCATGGTAAACGGGATCTAAAATGCCTGGTGGCT 1320

Qy 1321 TTTCACAAAAAGCAGATTTTCTTCATGTACTGTGATGTCTGATGCAATGCATCCTAGAAC 1380
Db 1321 TTTCACAAAAAGCAGATTTTCTTCATGTACTGTGATGTCTGATGCAATGCATCCTAGAAC 1380

Qy 1381 AAACTGGCCATTTGCTAGTTTACTCTAAAGACTAAACATAGTCTTGGTGTGTGTGGTCTT 1440
Db 1381 AAACTGGCCATTTGCTAGTTTACTCTAAAGACTAAACATAGTCTTGGTGTGTGTGGTCTT 1440

Qy 1441 ACTCATCTTCTAGTACCTTTAAGGACAAATCCTAAGGACTTGGACACTTGCAATAAAGAA 1500
Db 1441 ACTCATCTTCTAGTACCTTTAAGGACAAATCCTAAGGACTTGGACACTTGCAATAAAGAA 1500

Qy 1501 ATTTTATTTTAAACCCAAGCCTCCCTGGATTGATAATATATACACATTTGTCAGCATTTC 1560
Db 1501 ATTTTATTTTAAACCCAAGCCTCCCTGGATTGATAATATATACACATTTGTCAGCATTTC 1560

Qy 1561 CGGTCGTGGTGAGAGGCAGCTGTTTGAGCTCCAATATGTGCAGCTTTGAACTAGGGCTGG 1620
Db 1561 CGGTCGTGGTGAGAGGCAGCTGTTTGAGCTCCAATATGTGCAGCTTTGAACTAGGGCTGG 1620

Qy 1621 GGTTGTGGGTGCCTCTTCTGAAAGGTCTAACCATTATTGGATAACTGGCTTTTTTCTTCC 1680
Db 1621 GGTTGTGGGTGCCTCTTCTGAAAGGTCTAACCATTATTGGATAACTGGCTTTTTTCTTCC 1680

Qy 1681 TATGTCCTCTTTGGAATGTAACAATAAAAATAATTTTTGAAACATCAA 1728
Db 1681 TATGTCCTCTTTGGAATGTAACAATAAAAATAATTTTTGAAACATCAA 1728
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RESULT 5
AAF44254
ID   AAF44254 standard; cDNA; 1728 BP.
XX
AC   AAF44254;
XX
DT   02-APR-2001  (first entry)
XX
DE   Human PRO1375 (UNQ712) nucleotide sequence SEQ ID NO:417.
XX
KW   Human; secreted and transmembrane protein; PRO; cytostatic; cell death;
KW   cancer; chromosomal mapping; gene mapping; tissue typing;
KW   diagnostic assay; ss.
XX
OS   Homo sapiens.
XX
PN   WO200073454-A1.
XX
PD   07-DEC-2000.
XX
PF   30-MAR-2000; 2000WO-US008439.
XX
PR   02-JUN-1999;   99WO-US012252.
PR   23-JUN-1999;   99US-0141037P.
PR   07-JUL-1999;   99US-0143048P.
PR   20-JUL-1999;   99US-0144758P.
PR   26-JUL-1999;   99US-0145698P.
PR   28-JUL-1999;   99US-0146222P.
PR   17-AUG-1999;   99US-0149396P.
PR   15-SEP-1999;   99WO-US021090.
PR   15-SEP-1999;   99WO-US021547.
PR   08-OCT-1999;   99US-0158663P.
PR   30-NOV-1999;   99WO-US028313.
PR   01-DEC-1999;   99WO-US028301.
PR   16-DEC-1999;   99WO-US030095.
PR   20-DEC-1999;   99WO-US030911.
PR   05-JAN-2000; 2000WO-US000219.
PR   06-JAN-2000; 2000WO-US000376.
PR   11-FEB-2000; 2000WO-US003565.
PR   18-FEB-2000; 2000WO-US004341.
PR   22-FEB-2000; 2000WO-US004414.
PR   24-FEB-2000; 2000WO-US004914.
PR   24-FEB-2000; 2000WO-US005004.
PR   02-MAR-2000; 2000WO-US005841.
PR   15-MAR-2000; 2000WO-US006884.
PR   20-MAR-2000; 2000WO-US007377.
XX
PA   (GETH ) GENENTECH INC.
XX
PI   Ashkenazi AJ,  Baker KP,  Botstein D,  Desnoyers L,  Eaton DL;
PI   Ferrara N,  Fong S,  Gerber H,  Gerritsen ME,  Goddard A,  Godowski PJ;
PI   Grimaldi CJ,  Gurney AL,  Kljavin IJ,  Napier MA,  Pan J,  Paoni NF;
PI   Roy MA,  Stewart TA,  Tumas D,  Watanabe CK,  Williams PM,  Wood WI;
PI   Zhang Z;
XX
DR   WPI; 2001-032160/04.
DR   P-PSDB; AAB65285.
XX
PT   PRO polynucleotides used to produce polypeptides used to target bioactive
PT   molecules such as toxins, radiolabels or antibodies, to specific cells,
PT   to cause targeted cell death.
XX
PS   Claim 2; Fig 299; 935pp; English.
XX
CC   The present invention describes human secreted and transmembrane PRO
CC   proteins. The PRO proteins have cytostatic activity. The PRO proteins can
CC   be used for targeted delivery of bioactive molecules, such as toxins,
CC   radiolabels or antibodies, that cause cell death. PRO nucleotide
CC   sequences, and their fragments, can be used as hybridisation probes, in
CC   chromosomal and gene mapping, and in the generation of anti-sense RNA and
CC   DNA. They may also be used to produce transgenic animals which are used
CC   to develop and screen therapeutically useful reagents. The PRO nucleotide
CC   and protein sequence can be used for tissue typing and in treating
CC   cancer. Anti-PRO antibodies can be used in diagnostic assays. AAF44270 to
CC   AAF44470 represent PCR primers and hybridisation probes used in the
CC   isolation of human PRO sequences. AAF44087 to AAF44269 and AAB65154 to
CC   AAB65300 represent human PRO polynucleotide and protein sequences given
CC   in the exemplification of the present invention
XX
SQ   Sequence 1728 BP; 438 A; 360 C; 390 G; 540 T; 0 U; 0 Other;

  Query Match             100.0%;  Score 1728;  DB 5;  Length 1728;
  Best Local Similarity   100.0%;  Pred. No. 0;
  Matches 1728;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 CAGCCGGGTCCCAAGCCTGTGCCTGAGCCTGAGCCTGAGCCTGAGCCCGAGCCGGGAGCC 60
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Db          1 CAGCCGGGTCCCAAGCCTGTGCCTGAGCCTGAGCCTGAGCCTGAGCCCGAGCCGGGAGCC 60

Qy         61 GGTCGCGGGGGCTCCGGGCTGTGGGACCGCTGGGCCCCCAGCGATGGCGACCCTGTGGGG 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 GGTCGCGGGGGCTCCGGGCTGTGGGACCGCTGGGCCCCCAGCGATGGCGACCCTGTGGGG 120

Qy        121 AGGCCTTCTTCGGCTTGGCTCCTTGCTCAGCCTGTCGTGCCTGGCGCTTTCCGTGCTGCT 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 AGGCCTTCTTCGGCTTGGCTCCTTGCTCAGCCTGTCGTGCCTGGCGCTTTCCGTGCTGCT 180

Qy        181 GCTGGCGCAGCTGTCAGACGCCGCCAAGAATTTCGAGGATGTCAGATGTAAATGTATCTG 240
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Db        181 GCTGGCGCAGCTGTCAGACGCCGCCAAGAATTTCGAGGATGTCAGATGTAAATGTATCTG 240

Qy        241 CCCTCCCTATAAAGAAAATTCTGGGCATATTTATAATAAGAACATATCTCAGAAAGATTG 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 CCCTCCCTATAAAGAAAATTCTGGGCATATTTATAATAAGAACATATCTCAGAAAGATTG 300

Qy        301 TGATTGCCTTCATGTTGTGGAGCCCATGCCTGTGCGGGGGCCTGATGTAGAAGCATACTG 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 TGATTGCCTTCATGTTGTGGAGCCCATGCCTGTGCGGGGGCCTGATGTAGAAGCATACTG 360

Qy        361 TCTACGCTGTGAATGCAAATATGAAGAAAGAAGCTCTGTCACAATCAAGGTTACCATTAT 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 TCTACGCTGTGAATGCAAATATGAAGAAAGAAGCTCTGTCACAATCAAGGTTACCATTAT 420

Qy        421 AATTTATCTCTCCATTTTGGGCCTTCTACTTCTGTACATGGTATATCTTACTCTGGTTGA 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        421 AATTTATCTCTCCATTTTGGGCCTTCTACTTCTGTACATGGTATATCTTACTCTGGTTGA 480

Qy        481 GCCCATACTGAAGAGGCGCCTCTTTGGACATGCACAGTTGATACAGAGTGATGATGATAT 540
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        481 GCCCATACTGAAGAGGCGCCTCTTTGGACATGCACAGTTGATACAGAGTGATGATGATAT 540

Qy        541 TGGGGATCACCAGCCTTTTGCAAATGCACACGATGTGCTAGCCCGCTCCCGCAGTCGAGC 600
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        541 TGGGGATCACCAGCCTTTTGCAAATGCACACGATGTGCTAGCCCGCTCCCGCAGTCGAGC 600

Qy        601 CAACGTGCTGAACAAGGTAGAATATGCACAGCAGCGCTGGAAGCTTCAAGTCCAAGAGCA 660
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        601 CAACGTGCTGAACAAGGTAGAATATGCACAGCAGCGCTGGAAGCTTCAAGTCCAAGAGCA 660

Qy        661 GCGAAAGTCTGTCTTTGACCGGCATGTTGTCCTCAGCTAATTGGGAATTGAATTCAAGGT 720
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        661 GCGAAAGTCTGTCTTTGACCGGCATGTTGTCCTCAGCTAATTGGGAATTGAATTCAAGGT 720

Qy        721 GACTAGAAAGAAACAGGCAGACAACTGGAAAGAACTGACTGGGTTTTGCTGGGTTTCATT 780
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        721 GACTAGAAAGAAACAGGCAGACAACTGGAAAGAACTGACTGGGTTTTGCTGGGTTTCATT 780

Qy        781 TTAATACCTTGTTGATTTCACCAACTGTTGCTGGAAGATTCAAAACTGGAAGCAAAAACT 840
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        781 TTAATACCTTGTTGATTTCACCAACTGTTGCTGGAAGATTCAAAACTGGAAGCAAAAACT 840

Qy        841 TGCTTGATTTTTTTTTCTTGTTAACGTAATAATAGAGACATTTTTAAAAGCACACAGCTC 900
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Db        841 TGCTTGATTTTTTTTTCTTGTTAACGTAATAATAGAGACATTTTTAAAAGCACACAGCTC 900
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Qy        901 AAAGTCAGCCAATAAGTCTTTTCCTATTTGTGACTTTTACTAATAAAAATAAATCTGCCT 960
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        901 AAAGTCAGCCAATAAGTCTTTTCCTATTTGTGACTTTTACTAATAAAAATAAATCTGCCT 960

Qy        961 GTAAATTATCTTGAAGTCCTTTACCTGGAACAAGCACTCTCTTTTTCACCACATAGTTTT 1020
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        961 GTAAATTATCTTGAAGTCCTTTACCTGGAACAAGCACTCTCTTTTTCACCACATAGTTTT 1020

Qy       1021 AACTTGACTTTCAAGATAATTTTCAGGGTTTTTGTTGTTGTTGTTTTTTGTTTGTTTGTT 1080
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1021 AACTTGACTTTCAAGATAATTTTCAGGGTTTTTGTTGTTGTTGTTTTTTGTTTGTTTGTT 1080

Qy       1081 TTGGTGGGAGAGGGGAGGGATGCCTGGGAAGTGGTTAACAACTTTTTTCAAGTCACTTTA 1140
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1081 TTGGTGGGAGAGGGGAGGGATGCCTGGGAAGTGGTTAACAACTTTTTTCAAGTCACTTTA 1140

Qy       1141 CTAAACAAACTTTTGTAAATAGACCTTACCTTCTATTTTCGAGTTTCATTTATATTTTGC 1200
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1141 CTAAACAAACTTTTGTAAATAGACCTTACCTTCTATTTTCGAGTTTCATTTATATTTTGC 1200

Qy       1201 AGTGTAGCCAGCCTCATCAAAGAGCTGACTTACTCATTTGACTTTTGCACTGACTGTATT 1260
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Db       1201 AGTGTAGCCAGCCTCATCAAAGAGCTGACTTACTCATTTGACTTTTGCACTGACTGTATT 1260

Qy       1261 ATCTGGGTATCTGCTGTGTCTGCACTTCATGGTAAACGGGATCTAAAATGCCTGGTGGCT 1320
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1261 ATCTGGGTATCTGCTGTGTCTGCACTTCATGGTAAACGGGATCTAAAATGCCTGGTGGCT 1320

Qy       1321 TTTCACAAAAAGCAGATTTTCTTCATGTACTGTGATGTCTGATGCAATGCATCCTAGAAC 1380
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1321 TTTCACAAAAAGCAGATTTTCTTCATGTACTGTGATGTCTGATGCAATGCATCCTAGAAC 1380

Qy       1381 AAACTGGCCATTTGCTAGTTTACTCTAAAGACTAAACATAGTCTTGGTGTGTGTGGTCTT 1440
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Db       1381 AAACTGGCCATTTGCTAGTTTACTCTAAAGACTAAACATAGTCTTGGTGTGTGTGGTCTT 1440

Qy       1441 ACTCATCTTCTAGTACCTTTAAGGACAAATCCTAAGGACTTGGACACTTGCAATAAAGAA 1500
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Db       1441 ACTCATCTTCTAGTACCTTTAAGGACAAATCCTAAGGACTTGGACACTTGCAATAAAGAA 1500

Qy       1501 ATTTTATTTTAAACCCAAGCCTCCCTGGATTGATAATATATACACATTTGTCAGCATTTC 1560
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Db       1501 ATTTTATTTTAAACCCAAGCCTCCCTGGATTGATAATATATACACATTTGTCAGCATTTC 1560

Qy       1561 CGGTCGTGGTGAGAGGCAGCTGTTTGAGCTCCAATATGTGCAGCTTTGAACTAGGGCTGG 1620
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1561 CGGTCGTGGTGAGAGGCAGCTGTTTGAGCTCCAATATGTGCAGCTTTGAACTAGGGCTGG 1620

Qy       1621 GGTTGTGGGTGCCTCTTCTGAAAGGTCTAACCATTATTGGATAACTGGCTTTTTTCTTCC 1680
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Db       1621 GGTTGTGGGTGCCTCTTCTGAAAGGTCTAACCATTATTGGATAACTGGCTTTTTTCTTCC 1680

Qy       1681 TATGTCCTCTTTGGAATGTAACAATAAAAATAATTTTTGAAACATCAA 1728
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Db       1681 TATGTCCTCTTTGGAATGTAACAATAAAAATAATTTTTGAAACATCAA 1728
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RESULT 6
ABX77979
ID ABX77979 standard; cDNA; 1728 BP.
XX
AC ABX77979;
XX
DT 14-APR-2003 (first entry)
XX
DE Human PRO polynucleotide #132.
XX
KW Human; PRO; gene; ss; cytostatic; tumour; cancer; breast; lung; stomach;
KW liver; horse; cow; dog; cat; sheep; pig; goat; rabbit; ADEPT;
KW antibody-dependent enzyme mediated prodrug therapy.
XX
OS Homo sapiens.
XX

PN US2003027163-A1.
XX
PD 06-FEB-2003.
XX
PF 15-NOV-2001; 2001US-00997666.
XX
PR 16-JUN-1997; 97US-0049787P.
PR 17-OCT-1997; 97US-0062250P.
PR 05-NOV-1997; 97WO-US020069.
PR 12-NOV-1997; 97US-0065186P.
PR 13-NOV-1997; 97US-0065311P.
PR 24-NOV-1997; 97US-0066770P.
PR 25-FEB-1998; 98US-0075945P.
PR 20-MAR-1998; 98US-0078910P.
PR 28-APR-1998; 98US-0083322P.
PR 07-MAY-1998; 98US-0084600P.
PR 28-MAY-1998; 98US-0087106P.
PR 02-JUN-1998; 98US-0087607P.
PR 02-JUN-1998; 98US-0087609P.
PR 02-JUN-1998; 98US-0087759P.
PR 03-JUN-1998; 98US-0087827P.
PR 04-JUN-1998; 98US-0088021P.
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PR 05-JUN-1998; 98US-0088167P.
PR 05-JUN-1998; 98US-0088202P.
PR 05-JUN-1998; 98US-0088212P.
PR 05-JUN-1998; 98US-0088217P.
PR 09-JUN-1998; 98US-0088655P.
PR 10-JUN-1998; 98US-0088734P.
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PR 10-JUN-1998; 98US-0088810P.
PR 10-JUN-1998; 98US-0088824P.
PR 10-JUN-1998; 98US-0088826P.
PR 11-JUN-1998; 98US-0088858P.
PR 11-JUN-1998; 98US-0088861P.
PR 11-JUN-1998; 98US-0088876P.
PR 12-JUN-1998; 98US-0089105P.
PR 16-JUN-1998; 98US-0089440P.
PR 16-JUN-1998; 98US-0089512P.
PR 16-JUN-1998; 98US-0089514P.
PR 17-JUN-1998; 98US-0089532P.
PR 17-JUN-1998; 98US-0089538P.
PR 17-JUN-1998; 98US-0089598P.
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PR 17-JUN-1998; 98US-0089653P.
PR 18-JUN-1998; 98US-0089801P.
PR 18-JUN-1998; 98US-0089907P.
PR 18-JUN-1998; 98US-0089908P.
PR 19-JUN-1998; 98US-0089947P.
PR 19-JUN-1998; 98US-0089948P.
PR 19-JUN-1998; 98US-0089952P.
PR 22-JUN-1998; 98US-0090246P.
PR 22-JUN-1998; 98US-0090252P.
PR 22-JUN-1998; 98US-0090254P.
PR 23-JUN-1998; 98US-0090349P.
PR 23-JUN-1998; 98US-0090355P.
PR 24-JUN-1998; 98US-0090429P.
PR 24-JUN-1998; 98US-0090431P.
PR 24-JUN-1998; 98US-0090435P.
PR 24-JUN-1998; 98US-0090444P.
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PR 24-JUN-1998; 98US-0090540P.
PR 24-JUN-1998; 98US-0090542P.

PR 24-JUN-1998; 98US-0090557P.
PR 25-JUN-1998; 98US-0090676P.
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Query Match 100.0%; Score 1728; DB 7; Length 1728;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1728; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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DT 28-APR-2003 (first entry)
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DE Novel human secreted or transmembrane protein PRO1385 DNA.
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KW Human; PRO; hypertrophy of neonatal heart; angiogenesis; wound healing;
KW cardiac insufficiency disorder; cancer; tumour; immune response;
KW adrenal cortical capillary endothelial growth; c-fos induction;
KW vascular endothelial growth factor inhibition; VEGF inhibition;
KW endothelial cell growth inhibitor; T-lymphocytes stimulation;
KW retinal neurons cell survival; rod photoreceptor cell survival;
KW retinal disorder; retinitis pigmentosum; kidney disorder;
KW mammalian kidney mesangial cell proliferation; Berger disease;
KW dermatitis; herpetiformis; Crohn's disease; chondrocyte proliferation;
KW chondrocyte redifferentiation; sports injury; arthritis; gene; ds.
XX
OS Homo sapiens.
XX
PN US2002132252-A1.
XX
PD 19-SEP-2002.
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PF 14-NOV-2001; 2001US-00990442.
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PR 16-JUN-1997; 97US-0049787P.
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PR 29-JUN-2001; 2001WO-US021066.
PR 09-JUL-2001; 2001WO-US021735.
PR 28-AUG-2001; 2001US-00941992.
XX
PA (GETH) GENENTECH INC.
XX
PI Ashkenazi AJ, Baker KP, Botstein D, Desnoyers L, Eaton DL;
PI Ferrara N, Fong S, Gerber H, Gerritsen ME, Goddard A, Godowski PJ;
PI Grimaldi JC, Gurney AL, Kljavin IJ, Napier MA, Pan J, Paoni NF;
PI Roy MA, Stewart TA, Tumas D, Watanabe CK, Williams PM, Wood WI;
PI Zhang Z;

XX
DR WPI; 2003-247083/24.
DR P-PSDB; ABU59179.
XX
PT Novel isolated PRO polypeptides e.g., PRO826, PRO1068, PRO1184, PRO1346
PT and PRO1375, which stimulate proliferation of stimulated T-lymphocytes
PT are therapeutically useful for enhancing immune response and in cancer
PT treatments.
XX
PS Claim 2; Fig 301; 648pp; English.
XX
CC The invention describes an isolated human PRO polypeptide. The PRO
CC polypeptides are useful in detecting PRO polypeptides in a sample, in
CC linking a bioactive molecule to a cell expressing a PRO polypeptide, and
CC in modulating at least one biological activity of a cell expressing a PRO
CC polypeptide. PRO1312 stimulates hypertrophy of neonatal heart and is thus
CC useful for treating cardiac insufficiency disorders. PRO1154 and PRO1186
CC stimulate adrenal cortical capillary endothelial growth, and PRO536,
CC PRO943, PRO828, PRO826, PRO1068 or PRO535, PRO826, PRO819, PRO1126,
CC PRO1360 and PRO1387 induce c-fos in endothelial cells, and are thus
CC useful for treating conditions or disorders where angiogenesis would be
CC beneficial, e.g. wound healing and antagonist of this polypeptide are
CC useful for treating cancerous tumours. PRO812 inhibits vascular
CC endothelial growth factor (VEGF) stimulated proliferation of endothelial
CC cells and is thus useful for inhibiting endothelial cell growth in
CC mammals which would be beneficial in inhibiting tumour growth. PRO826,
CC PRO1068, PRO1184, PRO1346 and PRO1375 stimulate proliferation of
CC stimulated T-lymphocytes and are therapeutically useful for enhancing
CC immune response. PRO828, PRO826, PRO1068 or PRO1132 enhance survival of
CC retinal neurons cells (PRO1132 is also enhances survival/proliferation of
CC rod photoreceptor cells) and therefore are useful for treating retinal
CC disorders of injuries, e.g. retinitis pigmentosum, AMD. PRO819, PRO813
CC and PRO11066 induce proliferation of mammalian kidney mesangial cells,
CC and therefore are useful for treating kidney disorders associated with
CC decreased mesangial cell function such as Berger disease or other
CC nephropathies associated with dermatitis, herpetiformis or Crohn's
CC disease. PRO1310, PRO844, PRO1312, PRO1192 and PRO1387 induce the
CC proliferation and/or redifferentiation of chondrocytes in culture and are
CC thus useful for treating sports injuries, and arthritis. This sequence
CC represents a novel human PRO protein polynucleotide
XX
SQ Sequence 1728 BP; 438 A; 360 C; 390 G; 540 T; 0 U; 0 Other;

Query Match 100.0%; Score 1728; DB 7; Length 1728;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1728; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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DT 26-JUN-2003 (first entry)
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KW Human; ss; gene; PRO; secreted protein; transmembrane protein;
KW cardiac insufficiency disorders; angiogenesis; wound healing;
KW cancerous tumour; immune response; retinal disorder; sight loss;
KW retinitis pigmentosum; age-related macular degeneration; AMD;
KW kidney disorder; Berger disease; nephropathy; dermatitis; herpetiformis;
KW Crohn's disease; sports injury; arthritis.
XX
OS Homo sapiens.
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PD 13-FEB-2003.
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Db       1561 CGGTCGTGGTGAGAGGCAGCTGTTTGAGCTCCAATATGTGCAGCTTTGAACTAGGGCTGG 1620

Qy       1621 GGTTGTGGGTGCCTCTTCTGAAAGGTCTAACCATTATTGGATAACTGGCTTTTTTCTTCC 1680
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1621 GGTTGTGGGTGCCTCTTCTGAAAGGTCTAACCATTATTGGATAACTGGCTTTTTTCTTCC 1680

Qy       1681 TATGTCCTCTTTGGAATGTAACAATAAAAATAATTTTTGAAACATCAA 1728
              ||||||||||||||||||||||||||||||||||||||||||||||||
Db       1681 TATGTCCTCTTTGGAATGTAACAATAAAAATAATTTTTGAAACATCAA 1728
```

RESULT 9
ABX90368
ID ABX90368 standard; cDNA; 1728 BP.
XX
AC ABX90368;
XX
DT 01-MAY-2003 (first entry)
XX
DE Human secreted/transmembrane protein cDNA, #168.
XX
KW Human; gene; ss; PRO; secreted; transmembrane; signal peptide;
KW pharmaceutical; diagnostic; therapeutic; gene therapy.
XX
OS Homo sapiens.
XX
PN US2002160384-A1.
XX
PD 31-OCT-2002.
XX
PF 14-NOV-2001; 2001US-00992598.
XX
PR 16-JUN-1997; 97US-0049787P.
PR 17-OCT-1997; 97US-0062250P.

PR 05-NOV-1997; 97WO-US020069.
PR 12-NOV-1997; 97US-0065186P.
PR 13-NOV-1997; 97US-0065311P.
PR 24-NOV-1997; 97US-0066770P.
PR 25-FEB-1998; 98US-0075945P.
PR 20-MAR-1998; 98US-0078910P.
PR 28-APR-1998; 98US-0083322P.
PR 07-MAY-1998; 98US-0084600P.
PR 28-MAY-1998; 98US-0087106P.
PR 02-JUN-1998; 98US-0087607P.
PR 02-JUN-1998; 98US-0087609P.
PR 02-JUN-1998; 98US-0087759P.
PR 03-JUN-1998; 98US-0087827P.
PR 04-JUN-1998; 98US-0088021P.
PR 04-JUN-1998; 98US-0088025P.
PR 04-JUN-1998; 98US-0088026P.
PR 04-JUN-1998; 98US-0088028P.
PR 04-JUN-1998; 98US-0088029P.
PR 04-JUN-1998; 98US-0088030P.
PR 04-JUN-1998; 98US-0088033P.
PR 04-JUN-1998; 98US-0088326P.
PR 05-JUN-1998; 98US-0088167P.
PR 05-JUN-1998; 98US-0088202P.
PR 05-JUN-1998; 98US-0088212P.
PR 05-JUN-1998; 98US-0088217P.
PR 09-JUN-1998; 98US-0088655P.
PR 10-JUN-1998; 98US-0088734P.
PR 10-JUN-1998; 98US-0088738P.
PR 10-JUN-1998; 98US-0088742P.
PR 10-JUN-1998; 98US-0088810P.
PR 10-JUN-1998; 98US-0088824P.
PR 10-JUN-1998; 98US-0088826P.
PR 11-JUN-1998; 98US-0088858P.
PR 11-JUN-1998; 98US-0088861P.
PR 11-JUN-1998; 98US-0088876P.
PR 12-JUN-1998; 98US-0089105P.
PR 16-JUN-1998; 98US-0089440P.
PR 16-JUN-1998; 98US-0089512P.
PR 16-JUN-1998; 98US-0089514P.
PR 17-JUN-1998; 98US-0089532P.
PR 17-JUN-1998; 98US-0089538P.
PR 17-JUN-1998; 98US-0089598P.
PR 17-JUN-1998; 98US-0089599P.
PR 17-JUN-1998; 98US-0089600P.
PR 17-JUN-1998; 98US-0089653P.
PR 18-JUN-1998; 98US-0089801P.
PR 18-JUN-1998; 98US-0089907P.
PR 18-JUN-1998; 98US-0089908P.
PR 16-SEP-1998; 98WO-US019330.
PR 17-SEP-1998; 98WO-US019437.
PR 07-OCT-1998; 98WO-US021141.
PR 01-DEC-1998; 98WO-US025108.
PR 05-JAN-1999; 99WO-US000106.
PR 08-MAR-1999; 99WO-US005028.
PR 02-JUN-1999; 99WO-US012252.
PR 15-SEP-1999; 99WO-US021090.
PR 15-SEP-1999; 99WO-US021547.
PR 30-NOV-1999; 99WO-US028313.
PR 01-DEC-1999; 99WO-US028301.
PR 01-DEC-1999; 99WO-US028634.
PR 16-DEC-1999; 99WO-US030095.
PR 20-DEC-1999; 99WO-US030911.
PR 05-JAN-2000; 2000WO-US000219.
PR 06-JAN-2000; 2000WO-US000376.
PR 11-FEB-2000; 2000WO-US003565.
PR 18-FEB-2000; 2000WO-US004341.
PR 22-FEB-2000; 2000WO-US004414.
PR 24-FEB-2000; 2000WO-US004914.
PR 24-FEB-2000; 2000WO-US005004.
PR 02-MAR-2000; 2000WO-US005841.
PR 10-MAR-2000; 2000WO-US006319.
PR 15-MAR-2000; 2000WO-US006884.
PR 20-MAR-2000; 2000WO-US007377.
PR 30-MAR-2000; 2000WO-US008439.
PR 15-MAY-2000; 2000WO-US013358.
PR 17-MAY-2000; 2000WO-US013705.
PR 22-MAY-2000; 2000WO-US014042.
PR 30-MAY-2000; 2000WO-US014941.
PR 02-JUN-2000; 2000WO-US015264.
PR 28-JUL-2000; 2000WO-US020710.
PR 11-AUG-2000; 2000WO-US022031.
PR 23-AUG-2000; 2000WO-US023522.
PR 24-AUG-2000; 2000WO-US023328.
PR 08-NOV-2000; 2000WO-US030952.
PR 01-DEC-2000; 2000WO-US032678.
PR 28-FEB-2001; 2001WO-US006520.
PR 01-JUN-2001; 2001WO-US017800.
PR 20-JUN-2001; 2001WO-US019692.
PR 29-JUN-2001; 2001WO-US021066.
PR 09-JUL-2001; 2001WO-US021735.
PR 28-AUG-2001; 2001US-00941992.
XX
PA (GETH) GENENTECH INC.
XX
PI Ashkenazi AJ, Baker KP, Botstein D, Desnoyers L, Eaton DL;
PI Ferrara N, Fong S, Gerber H, Gerritsen ME, Goddard A, Godowski PJ;
PI Grimaldi JC, Gurney AL, Kljavin IJ, Napier MA, Pan J, Paoni NF;
PI Roy MA, Stewart TA, Tumas D, Watanabe CK, Williams PM, Wood WI;
PI Zhang Z;
XX
DR WPI; 2003-288106/28.
DR P-PSDB; ABU60609.
XX
PT New transmembrane polypeptides and nucleic acids encoding the
PT polypeptides, useful in gene therapy, in chromosome identification, as
PT chromosome markers, or in generating probes.
XX
PS Claim 2; Fig 299; 650pp; English.
XX
CC The invention discloses isolated PRO secreted/transmembrane polypeptides
CC comprising a sequence without signal peptide and the nucleic acid
CC encoding them. The polypeptides can be used to raise antibodies that
CC specifically bind to the PRO polypeptide, for linking a bioactive
CC molecule to a cell expressing a PRO protein and for modulating at least
CC one biological activity of a cell. The PRO polypeptides or
CC polynucleotides are also useful in gene therapy, in chromosome
CC identification, as chromosome markers, or in generating probes. The PRO
CC polypeptides are useful as molecular markers for protein electrophoresis,
CC and the isolated nucleic acids may be used for recombinantly expressing
CC those markers. The PRO polypeptides and nucleic acids may also be used in
CC tissue typing. Anti-PRO antibodies are useful in diagnostic assays for
CC PRO, and in affinity purification of PRO from recombinant cell culture or
CC natural sources. The sequences presented in ABX90083-ABX90468 are the
CC genes encoding, the primers amplifying and the probes detecting the PRO
CC polynucleotides of the invention. Note: The sequence data for this patent
CC is also available in electronic format from USPTO at
CC seqdata.uspto.gov/sequence.html
XX
SQ Sequence 1728 BP; 438 A; 360 C; 390 G; 540 T; 0 U; 0 Other;

Query Match 100.0%; Score 1728; DB 7; Length 1728;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1728; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CAGCCGGGTCCCAAGCCTGTGCCTGAGCCTGAGCCTGAGCCTGAGCCCGAGCCGGGAGCC 60
Db 1 CAGCCGGGTCCCAAGCCTGTGCCTGAGCCTGAGCCTGAGCCTGAGCCCGAGCCGGGAGCC 60

Qy 61 GGTCGCGGGGGCTCCGGGCTGTGGGACCGCTGGGCCCCCAGCGATGGCGACCCTGTGGGG 120
Db 61 GGTCGCGGGGGCTCCGGGCTGTGGGACCGCTGGGCCCCCAGCGATGGCGACCCTGTGGGG 120

Qy 121 AGGCCTTCTTCGGCTTGGCTCCTTGCTCAGCCTGTCGTGCCTGGCGCTTTCCGTGCTGCT 180
Db 121 AGGCCTTCTTCGGCTTGGCTCCTTGCTCAGCCTGTCGTGCCTGGCGCTTTCCGTGCTGCT 180

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Qy       181 GCTGGCGCAGCTGTCAGACGCCGCCAAGAATTTCGAGGATGTCAGATGTAAATGTATCTG 240
Db       181 GCTGGCGCAGCTGTCAGACGCCGCCAAGAATTTCGAGGATGTCAGATGTAAATGTATCTG 240

Qy       241 CCCTCCCTATAAAGAAAATTCTGGGCATATTTATAATAAGAACATATCTCAGAAAGATTG 300
Db       241 CCCTCCCTATAAAGAAAATTCTGGGCATATTTATAATAAGAACATATCTCAGAAAGATTG 300

Qy       301 TGATTGCCTTCATGTTGTGGAGCCCATGCCTGTGCGGGGGCCTGATGTAGAAGCATACTG 360
Db       301 TGATTGCCTTCATGTTGTGGAGCCCATGCCTGTGCGGGGGCCTGATGTAGAAGCATACTG 360

Qy       361 TCTACGCTGTGAATGCAAATATGAAGAAAGAAGCTCTGTCACAATCAAGGTTACCATTAT 420
Db       361 TCTACGCTGTGAATGCAAATATGAAGAAAGAAGCTCTGTCACAATCAAGGTTACCATTAT 420

Qy       421 AATTTATCTCTCCATTTTGGGCCTTCTACTTCTGTACATGGTATATCTTACTCTGGTTGA 480
Db       421 AATTTATCTCTCCATTTTGGGCCTTCTACTTCTGTACATGGTATATCTTACTCTGGTTGA 480

Qy       481 GCCCATACTGAAGAGGCGCCTCTTTGGACATGCACAGTTGATACAGAGTGATGATGATAT 540
Db       481 GCCCATACTGAAGAGGCGCCTCTTTGGACATGCACAGTTGATACAGAGTGATGATGATAT 540

Qy       541 TGGGGATCACCAGCCTTTTGCAAATGCACACGATGTGCTAGCCCGCTCCCGCAGTCGAGC 600
Db       541 TGGGGATCACCAGCCTTTTGCAAATGCACACGATGTGCTAGCCCGCTCCCGCAGTCGAGC 600

Qy       601 CAACGTGCTGAACAAGGTAGAATATGCACAGCAGCGCTGGAAGCTTCAAGTCCAAGAGCA 660
Db       601 CAACGTGCTGAACAAGGTAGAATATGCACAGCAGCGCTGGAAGCTTCAAGTCCAAGAGCA 660

Qy       661 GCGAAAGTCTGTCTTTGACCGGCATGTTGTCCTCAGCTAATTGGGAATTGAATTCAAGGT 720
Db       661 GCGAAAGTCTGTCTTTGACCGGCATGTTGTCCTCAGCTAATTGGGAATTGAATTCAAGGT 720

Qy       721 GACTAGAAAGAAACAGGCAGACAACTGGAAAGAACTGACTGGGTTTTGCTGGGTTTCATT 780
Db       721 GACTAGAAAGAAACAGGCAGACAACTGGAAAGAACTGACTGGGTTTTGCTGGGTTTCATT 780

Qy       781 TTAATACCTTGTTGATTTCACCAACTGTTGCTGGAAGATTCAAAACTGGAAGCAAAAACT 840
Db       781 TTAATACCTTGTTGATTTCACCAACTGTTGCTGGAAGATTCAAAACTGGAAGCAAAAACT 840

Qy       841 TGCTTGATTTTTTTTTCTTGTTAACGTAATAATAGAGACATTTTTAAAAGCACACAGCTC 900
Db       841 TGCTTGATTTTTTTTTCTTGTTAACGTAATAATAGAGACATTTTTAAAAGCACACAGCTC 900

Qy       901 AAAGTCAGCCAATAAGTCTTTTCCTATTTGTGACTTTTACTAATAAAAATAAATCTGCCT 960
Db       901 AAAGTCAGCCAATAAGTCTTTTCCTATTTGTGACTTTTACTAATAAAAATAAATCTGCCT 960

Qy       961 GTAAATTATCTTGAAGTCCTTTACCTGGAACAAGCACTCTCTTTTTCACCACATAGTTTT 1020
Db       961 GTAAATTATCTTGAAGTCCTTTACCTGGAACAAGCACTCTCTTTTTCACCACATAGTTTT 1020

Qy      1021 AACTTGACTTTCAAGATAATTTTCAGGGTTTTTGTTGTTGTTGTTTTTTGTTTGTTTGTT 1080
Db      1021 AACTTGACTTTCAAGATAATTTTCAGGGTTTTTGTTGTTGTTGTTTTTTGTTTGTTTGTT 1080

Qy      1081 TTGGTGGGAGAGGGGAGGGATGCCTGGGAAGTGGTTAACAACTTTTTTCAAGTCACTTTA 1140
Db      1081 TTGGTGGGAGAGGGGAGGGATGCCTGGGAAGTGGTTAACAACTTTTTTCAAGTCACTTTA 1140

Qy      1141 CTAAACAAACTTTTGTAAATAGACCTTACCTTCTATTTTCGAGTTTCATTTATATTTTGC 1200
Db      1141 CTAAACAAACTTTTGTAAATAGACCTTACCTTCTATTTTCGAGTTTCATTTATATTTTGC 1200

Qy      1201 AGTGTAGCCAGCCTCATCAAAGAGCTGACTTACTCATTTGACTTTTGCACTGACTGTATT 1260
Db      1201 AGTGTAGCCAGCCTCATCAAAGAGCTGACTTACTCATTTGACTTTTGCACTGACTGTATT 1260

Qy      1261 ATCTGGGTATCTGCTGTGTCTGCACTTCATGGTAAACGGGATCTAAAATGCCTGGTGGCT 1320
Db      1261 ATCTGGGTATCTGCTGTGTCTGCACTTCATGGTAAACGGGATCTAAAATGCCTGGTGGCT 1320

Qy      1321 TTTCACAAAAAGCAGATTTTCTTCATGTACTGTGATGTCTGATGCAATGCATCCTAGAAC 1380
Db      1321 TTTCACAAAAAGCAGATTTTCTTCATGTACTGTGATGTCTGATGCAATGCATCCTAGAAC 1380

Qy      1381 AAACTGGCCATTTGCTAGTTTACTCTAAAGACTAAACATAGTCTTGGTGTGTGTGGTCTT 1440
Db      1381 AAACTGGCCATTTGCTAGTTTACTCTAAAGACTAAACATAGTCTTGGTGTGTGTGGTCTT 1440

Qy      1441 ACTCATCTTCTAGTACCTTTAAGGACAAATCCTAAGGACTTGGACACTTGCAATAAAGAA 1500
Db      1441 ACTCATCTTCTAGTACCTTTAAGGACAAATCCTAAGGACTTGGACACTTGCAATAAAGAA 1500

Qy      1501 ATTTTATTTTAAACCCAAGCCTCCCTGGATTGATAATATATACACATTTGTCAGCATTTC 1560
Db      1501 ATTTTATTTTAAACCCAAGCCTCCCTGGATTGATAATATATACACATTTGTCAGCATTTC 1560

Qy      1561 CGGTCGTGGTGAGAGGCAGCTGTTTGAGCTCCAATATGTGCAGCTTTGAACTAGGGCTGG 1620
Db      1561 CGGTCGTGGTGAGAGGCAGCTGTTTGAGCTCCAATATGTGCAGCTTTGAACTAGGGCTGG 1620

Qy      1621 GGTTGTGGGTGCCTCTTCTGAAAGGTCTAACCATTATTGGATAACTGGCTTTTTTCTTCC 1680
Db      1621 GGTTGTGGGTGCCTCTTCTGAAAGGTCTAACCATTATTGGATAACTGGCTTTTTTCTTCC 1680

Qy      1681 TATGTCCTCTTTGGAATGTAACAATAAAAATAATTTTTGAAACATCAA 1728
Db      1681 TATGTCCTCTTTGGAATGTAACAATAAAAATAATTTTTGAAACATCAA 1728
```

RESULT 10
ABX64214
ID ABX64214 standard; cDNA; 1728 BP.
XX
AC ABX64214;
XX
DT 26-FEB-2003 (first entry)
XX
DE cDNA encoding human PRO1375 polypeptide.
XX
KW Human; PRO polypeptide; secreted protein; transmembrane protein;
KW genetic disorder; antibacterial; immunosuppressive; transgenic;
KW gene therapy; gene; ss.
XX
OS Homo sapiens.
XX
PN US2002103125-A1.
XX
PD 01-AUG-2002.
XX
PF 20-NOV-2001; 2001US-00989731.
XX
PR 16-JUN-1997; 97US-0049787P.
PR 17-OCT-1997; 97US-0062250P.
PR 05-NOV-1997; 97WO-US020069.
PR 12-NOV-1997; 97US-0065186P.
PR 13-NOV-1997; 97US-0065311P.
PR 24-NOV-1997; 97US-0066770P.
PR 25-FEB-1998; 98US-0075945P.
PR 20-MAR-1998; 98US-0078910P.
PR 28-APR-1998; 98US-0083322P.
PR 07-MAY-1998; 98US-0084600P.
PR 28-MAY-1998; 98US-0087106P.
PR 02-JUN-1998; 98US-0087607P.
PR 02-JUN-1998; 98US-0087609P.
PR 02-JUN-1998; 98US-0087759P.
PR 03-JUN-1998; 98US-0087827P.
PR 04-JUN-1998; 98US-0088021P.
PR 04-JUN-1998; 98US-0088025P.
PR 04-JUN-1998; 98US-0088026P.
PR 04-JUN-1998; 98US-0088028P.

PR 04-JUN-1998; 98US-0088029P.
PR 04-JUN-1998; 98US-0088030P.
PR 04-JUN-1998; 98US-0088033P.
PR 04-JUN-1998; 98US-0088326P.
PR 05-JUN-1998; 98US-0088167P.
PR 05-JUN-1998; 98US-0088202P.
PR 05-JUN-1998; 98US-0088212P.
PR 05-JUN-1998; 98US-0088217P.
PR 09-JUN-1998; 98US-0088655P.
PR 10-JUN-1998; 98US-0088734P.
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PR 10-JUN-1998; 98US-0088826P.
PR 11-JUN-1998; 98US-0088858P.
PR 11-JUN-1998; 98US-0088861P.
PR 11-JUN-1998; 98US-0088876P.
PR 12-JUN-1998; 98US-0089105P.
PR 16-JUN-1998; 98US-0089440P.
PR 16-JUN-1998; 98US-0089512P.
PR 16-JUN-1998; 98US-0089514P.
PR 17-JUN-1998; 98US-0089532P.
PR 17-JUN-1998; 98US-0089538P.
PR 17-JUN-1998; 98US-0089598P.
PR 17-JUN-1998; 98US-0089599P.
PR 17-JUN-1998; 98US-0089600P.
PR 17-JUN-1998; 98US-0089653P.
PR 18-JUN-1998; 98US-0089801P.
PR 18-JUN-1998; 98US-0089907P.
PR 18-JUN-1998; 98US-0089908P.
PR 16-SEP-1998; 98WO-US019330.
PR 17-SEP-1998; 98WO-US019437.
PR 07-OCT-1998; 98WO-US021141.
PR 01-DEC-1998; 98WO-US025108.
PR 05-JAN-1999; 99WO-US000106.
PR 08-MAR-1999; 99WO-US005028.
PR 02-JUN-1999; 99WO-US012252.
PR 15-SEP-1999; 99WO-US021090.
PR 15-SEP-1999; 99WO-US021547.
PR 30-NOV-1999; 99WO-US028313.
PR 01-DEC-1999; 99WO-US028301.
PR 01-DEC-1999; 99WO-US028634.
PR 16-DEC-1999; 99WO-US030095.
PR 20-DEC-1999; 99WO-US030911.
PR 06-JAN-2000; 2000WO-US000219.
PR 06-JAN-2000; 2000WO-US000376.
PR 11-FEB-2000; 2000WO-US003565.
PR 18-FEB-2000; 2000WO-US004341.
PR 22-FEB-2000; 2000WO-US004414.
PR 24-FEB-2000; 2000WO-US004914.
PR 24-FEB-2000; 2000WO-US005004.
PR 02-MAR-2000; 2000WO-US005841.
PR 10-MAR-2000; 2000WO-US006319.
PR 15-MAR-2000; 2000WO-US006884.
PR 20-MAR-2000; 2000WO-US007377.
PR 30-MAR-2000; 2000WO-US008439.
PR 15-MAY-2000; 2000WO-US013358.
PR 17-MAY-2000; 2000WO-US013705.
PR 22-MAY-2000; 2000WO-US014042.
PR 30-MAY-2000; 2000WO-US014941.
PR 02-JUN-2000; 2000WO-US015264.
PR 28-JUL-2000; 2000WO-US020710.
PR 11-AUG-2000; 2000WO-US022031.
PR 23-AUG-2000; 2000WO-US023522.
PR 24-AUG-2000; 2000WO-US023328.
PR 08-NOV-2000; 2000WO-US030952.
PR 01-DEC-2000; 2000WO-US032678.
PR 28-FEB-2001; 2001WO-US006520.
PR 01-JUN-2001; 2001WO-US017800.
PR 20-JUN-2001; 2001WO-US019692.
PR 29-JUN-2001; 2001WO-US021066.
PR 09-JUL-2001; 2001WO-US021735.

PR 28-AUG-2001; 2001US-00941992.
XX
PA (GETH) GENENTECH LTD.
XX
PI Ashkenazi AJ, Baker KP, Botstein D, Desnoyers L, Eaton DL;
PI Ferrara N, Fong S, Gerber H, Gerritsen ME, Goddard A, Godowski PJ;
PI Grimaldi JC, Gurney AL, Kljavin IJ, Napier MA, Pan J, Paoni NF;
PI Roy MA, Stewart TA, Tumas D, Watanabe CK, Williams PM, Wood WI;
PI Zhang Z;
XX
DR WPI; 2003-102117/09.
DR P-PSDB; ABU13991.
XX
PT Novel secreted and transmembrane polypeptide for modulating biological
PT activity of cell expressing the polypeptide, identifying agonists or
PT antagonists of polypeptide, and as molecular weight markers.
XX
PS Claim 2; Fig 299; 649pp; English.
XX
CC The present invention relates to the isolation of novel human PRO
CC polypeptides, and the polynucleotide sequences encoding them. The PRO
CC polypeptides are secreted and transmembrane proteins. The PRO
CC polypeptides are useful for detecting other PRO polypeptides, for linking
CC bioactive molecules to cells expressing PRO polypeptides, for modulating
CC biological activities of cells expressing PRO polypeptides, and for for
CC identifying agonists or antagonists. The polynucleotide sequences
CC encoding PRO polypeptides are useful as hybridisation probes, in
CC chromosome and gene mapping, in the generation of antisense RNA and DNA,
CC in the preparation of PRO polypeptides, for generating transgenic animals
CC or knockout animals, to construct hybridisation probes for mapping the
CC gene which encodes the PRO polypeptide, and for the genetic analysis of
CC individuals with genetic disorders, in gene therapy, for chromosome
CC identification, as chromosome markers, and for generating probes for PCR,
CC Northern analysis, Southern analysis and Western analysis. The present
CC sequence encodes a human PRO polypeptide of the invention. Note: The
CC sequence data for this patent was obtained in electronic format directly
CC from the USPTO web site at seqdata.uspto.gov/psipsDIDEntry.html
XX
SQ Sequence 1728 BP; 438 A; 360 C; 390 G; 540 T; 0 U; 0 Other;

Query Match 100.0%; Score 1728; DB 7; Length 1728;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1728; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CAGCCGGGTCCCAAGCCTGTGCCTGAGCCTGAGCCTGAGCCTGAGCCCGAGCCGGGAGCC 60
Db 1 CAGCCGGGTCCCAAGCCTGTGCCTGAGCCTGAGCCTGAGCCTGAGCCCGAGCCGGGAGCC 60

Qy 61 GGTCGCGGGGGCTCCGGGCTGTGGGACCGCTGGGCCCCCAGCGATGGCGACCCTGTGGGG 120
Db 61 GGTCGCGGGGGCTCCGGGCTGTGGGACCGCTGGGCCCCCAGCGATGGCGACCCTGTGGGG 120

Qy 121 AGGCCTTCTTCGGCTTGGCTCCTTGCTCAGCCTGTCGTGCCTGGCGCTTTCCGTGCTGCT 180
Db 121 AGGCCTTCTTCGGCTTGGCTCCTTGCTCAGCCTGTCGTGCCTGGCGCTTTCCGTGCTGCT 180

Qy 181 GCTGGCGCAGCTGTCAGACGCCGCCAAGAATTTCGAGGATGTCAGATGTAAATGTATCTG 240
Db 181 GCTGGCGCAGCTGTCAGACGCCGCCAAGAATTTCGAGGATGTCAGATGTAAATGTATCTG 240

Qy 241 CCCTCCCTATAAAGAAAATTCTGGGCATATTTATAATAAGAACATATCTCAGAAAGATTG 300
Db 241 CCCTCCCTATAAAGAAAATTCTGGGCATATTTATAATAAGAACATATCTCAGAAAGATTG 300

Qy 301 TGATTGCCTTCATGTTGTGGAGCCCATGCCTGTGCGGGGGCCTGATGTAGAAGCATACTG 360
Db 301 TGATTGCCTTCATGTTGTGGAGCCCATGCCTGTGCGGGGGCCTGATGTAGAAGCATACTG 360

Qy 361 TCTACGCTGTGAATGCAAATATGAAGAAAGAAGCTCTGTCACAATCAAGGTTACCATTAT 420
Db 361 TCTACGCTGTGAATGCAAATATGAAGAAAGAAGCTCTGTCACAATCAAGGTTACCATTAT 420

Qy 421 AATTTATCTCTCCATTTTGGGCCTTCTACTTCTGTACATGGTATATCTTACTCTGGTTGA 480

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Db        421 AATTTATCTCTCCATTTTGGGCCTTCTACTTCTGTACATGGTATATCTTACTCTGGTTGA 480

Qy        481 GCCCATACTGAAGAGGCGCCTCTTTGGACATGCACAGTTGATACAGAGTGATGATGATAT 540
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        481 GCCCATACTGAAGAGGCGCCTCTTTGGACATGCACAGTTGATACAGAGTGATGATGATAT 540

Qy        541 TGGGGATCACCAGCCTTTTGCAAATGCACACGATGTGCTAGCCCGCTCCCGCAGTCGAGC 600
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        541 TGGGGATCACCAGCCTTTTGCAAATGCACACGATGTGCTAGCCCGCTCCCGCAGTCGAGC 600

Qy        601 CAACGTGCTGAACAAGGTAGAATATGCACAGCAGCGCTGGAAGCTTCAAGTCCAAGAGCA 660
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        601 CAACGTGCTGAACAAGGTAGAATATGCACAGCAGCGCTGGAAGCTTCAAGTCCAAGAGCA 660

Qy        661 GCGAAAGTCTGTCTTTGACCGGCATGTTGTCCTCAGCTAATTGGGAATTGAATTCAAGGT 720
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        661 GCGAAAGTCTGTCTTTGACCGGCATGTTGTCCTCAGCTAATTGGGAATTGAATTCAAGGT 720

Qy        721 GACTAGAAAGAAACAGGCAGACAACTGGAAAGAACTGACTGGGTTTTGCTGGGTTTCATT 780
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        721 GACTAGAAAGAAACAGGCAGACAACTGGAAAGAACTGACTGGGTTTTGCTGGGTTTCATT 780

Qy        781 TTAATACCTTGTTGATTTCACCAACTGTTGCTGGAAGATTCAAAACTGGAAGCAAAAACT 840
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Db        781 TTAATACCTTGTTGATTTCACCAACTGTTGCTGGAAGATTCAAAACTGGAAGCAAAAACT 840

Qy        841 TGCTTGATTTTTTTTTCTTGTTAACGTAATAATAGAGACATTTTTAAAAGCACACAGCTC 900
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Db        841 TGCTTGATTTTTTTTTCTTGTTAACGTAATAATAGAGACATTTTTAAAAGCACACAGCTC 900

Qy        901 AAAGTCAGCCAATAAGTCTTTTCCTATTTGTGACTTTTACTAATAAAAATAAATCTGCCT 960
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Db        901 AAAGTCAGCCAATAAGTCTTTTCCTATTTGTGACTTTTACTAATAAAAATAAATCTGCCT 960

Qy        961 GTAAATTATCTTGAAGTCCTTTACCTGGAACAAGCACTCTCTTTTTCACCACATAGTTTT 1020
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Db        961 GTAAATTATCTTGAAGTCCTTTACCTGGAACAAGCACTCTCTTTTTCACCACATAGTTTT 1020

Qy       1021 AACTTGACTTTCAAGATAATTTTCAGGGTTTTTGTTGTTGTTGTTTTTTGTTTGTTTGTT 1080
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Db       1021 AACTTGACTTTCAAGATAATTTTCAGGGTTTTTGTTGTTGTTGTTTTTTGTTTGTTTGTT 1080

Qy       1081 TTGGTGGGAGAGGGGAGGGATGCCTGGGAAGTGGTTAACAACTTTTTTCAAGTCACTTTA 1140
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Db       1081 TTGGTGGGAGAGGGGAGGGATGCCTGGGAAGTGGTTAACAACTTTTTTCAAGTCACTTTA 1140

Qy       1141 CTAAACAAACTTTTGTAAATAGACCTTACCTTCTATTTTCGAGTTTCATTTATATTTTGC 1200
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Db       1141 CTAAACAAACTTTTGTAAATAGACCTTACCTTCTATTTTCGAGTTTCATTTATATTTTGC 1200

Qy       1201 AGTGTAGCCAGCCTCATCAAAGAGCTGACTTACTCATTTGACTTTTGCACTGACTGTATT 1260
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Qy       1261 ATCTGGGTATCTGCTGTGTCTGCACTTCATGGTAAACGGGATCTAAAATGCCTGGTGGCT 1320
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Db       1261 ATCTGGGTATCTGCTGTGTCTGCACTTCATGGTAAACGGGATCTAAAATGCCTGGTGGCT 1320

Qy       1321 TTTCACAAAAAGCAGATTTTCTTCATGTACTGTGATGTCTGATGCAATGCATCCTAGAAC 1380
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Db       1321 TTTCACAAAAAGCAGATTTTCTTCATGTACTGTGATGTCTGATGCAATGCATCCTAGAAC 1380

Qy       1381 AAACTGGCCATTTGCTAGTTTACTCTAAAGACTAAACATAGTCTTGGTGTGTGTGGTCTT 1440
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Qy       1441 ACTCATCTTCTAGTACCTTTAAGGACAAATCCTAAGGACTTGGACACTTGCAATAAAGAA 1500
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Qy       1501 ATTTTATTTTAAACCCAAGCCTCCCTGGATTGATAATATATACACATTTGTCAGCATTTC 1560
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Db       1501 ATTTTATTTTAAACCCAAGCCTCCCTGGATTGATAATATATACACATTTGTCAGCATTTC 1560

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Qy       1621 GGTTGTGGGTGCCTCTTCTGAAAGGTCTAACCATTATTGGATAACTGGCTTTTTTCTTCC 1680
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1621 GGTTGTGGGTGCCTCTTCTGAAAGGTCTAACCATTATTGGATAACTGGCTTTTTTCTTCC 1680

Qy       1681 TATGTCCTCTTTGGAATGTAACAATAAAAATAATTTTTGAAACATCAA 1728
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Db       1681 TATGTCCTCTTTGGAATGTAACAATAAAAATAATTTTTGAAACATCAA 1728
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RESULT 11
ACA64436
ID ACA64436 standard; cDNA; 1728 BP.
XX
AC ACA64436;
XX
DT 17-JUN-2003 (first entry)
XX
DE Novel human secreted and transmembrane protein PRO1375 cDNA.
XX
KW Human; secreted and transmembrane protein; cytostatic; anti-HIV;
KW virucide; hepatotropic; antiinflammatory; neuroprotective; gene therapy;
KW PRO; pharmaceutical; diagnostic; biosensor; bioreactor; malignancy;
KW cancer; ovarian cancer; colorectal cancer; Kaposi's sarcoma; leukaemia;
KW lymphoma; hepatitis B; multiple sclerosis; Crohn's disease;
KW drug screening; gene; ss.
XX
OS Homo sapiens.
XX
PN US2003003531-A1.
XX
PD 02-JAN-2003.
XX
PF 19-NOV-2001; 2001US-00989734.
XX
PR 16-JUN-1997; 97US-0049787P.
PR 17-OCT-1997; 97US-0062250P.
PR 05-NOV-1997; 97WO-US020069.
PR 12-NOV-1997; 97US-0065186P.
PR 13-NOV-1997; 97US-0065311P.
PR 24-NOV-1997; 97US-0066770P.
PR 25-FEB-1998; 98US-0075945P.
PR 20-MAR-1998; 98US-0078910P.
PR 28-APR-1998; 98US-0083322P.
PR 07-MAY-1998; 98US-0084600P.
PR 28-MAY-1998; 98US-0087106P.
PR 02-JUN-1998; 98US-0087607P.
PR 02-JUN-1998; 98US-0087609P.
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PR 03-JUN-1998; 98US-0087827P.
PR 04-JUN-1998; 98US-0088021P.
PR 04-JUN-1998; 98US-0088025P.
PR 04-JUN-1998; 98US-0088026P.
PR 04-JUN-1998; 98US-0088028P.
PR 04-JUN-1998; 98US-0088029P.
PR 04-JUN-1998; 98US-0088030P.
PR 04-JUN-1998; 98US-0088033P.
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PR 05-JUN-1998; 98US-0088212P.
PR 05-JUN-1998; 98US-0088217P.
PR 09-JUN-1998; 98US-0088655P.
PR 10-JUN-1998; 98US-0088734P.
PR 10-JUN-1998; 98US-0088738P.
PR 10-JUN-1998; 98US-0088742P.
PR 10-JUN-1998; 98US-0088810P.
PR 10-JUN-1998; 98US-0088824P.

PR 10-JUN-1998; 98US-0088826P.
PR 11-JUN-1998; 98US-0088858P.
PR 11-JUN-1998; 98US-0088861P.
PR 11-JUN-1998; 98US-0088876P.
PR 12-JUN-1998; 98US-0089105P.
PR 16-JUN-1998; 98US-0089440P.
PR 16-JUN-1998; 98US-0089512P.
PR 16-JUN-1998; 98US-0089514P.
PR 17-JUN-1998; 98US-0089532P.
PR 17-JUN-1998; 98US-0089538P.
PR 17-JUN-1998; 98US-0089598P.
PR 17-JUN-1998; 98US-0089599P.
PR 17-JUN-1998; 98US-0089600P.
PR 17-JUN-1998; 98US-0089653P.
PR 18-JUN-1998; 98US-0089801P.
PR 18-JUN-1998; 98US-0089907P.
PR 18-JUN-1998; 98US-0089908P.
PR 16-SEP-1998; 98WO-US019330.
PR 17-SEP-1998; 98WO-US019437.
PR 07-OCT-1998; 98WO-US021141.
PR 01-DEC-1998; 98WO-US025108.
PR 05-JAN-1999; 99WO-US000106.
PR 08-MAR-1999; 99WO-US005028.
PR 02-JUN-1999; 99WO-US012252.
PR 15-SEP-1999; 99WO-US021090.
PR 15-SEP-1999; 99WO-US021547.
PR 30-NOV-1999; 99WO-US028313.
PR 01-DEC-1999; 99WO-US028301.
PR 01-DEC-1999; 99WO-US028634.
PR 16-DEC-1999; 99WO-US030095.
PR 20-DEC-1999; 99WO-US030911.
PR 05-JAN-2000; 2000WO-US000219.
PR 06-JAN-2000; 2000WO-US000376.
PR 11-FEB-2000; 2000WO-US003565.
PR 18-FEB-2000; 2000WO-US004341.
PR 22-FEB-2000; 2000WO-US004414.
PR 24-FEB-2000; 2000WO-US004914.
PR 24-FEB-2000; 2000WO-US005004.
PR 02-MAR-2000; 2000WO-US005841.
PR 10-MAR-2000; 2000WO-US006319.
PR 15-MAR-2000; 2000WO-US006884.
PR 20-MAR-2000; 2000WO-US007377.
PR 30-MAR-2000; 2000WO-US008439.
PR 15-MAY-2000; 2000WO-US013358.
PR 17-MAY-2000; 2000WO-US013705.
PR 22-MAY-2000; 2000WO-US014042.
PR 30-MAY-2000; 2000WO-US014941.
PR 02-JUN-2000; 2000WO-US015264.
PR 28-JUL-2000; 2000WO-US020710.
PR 11-AUG-2000; 2000WO-US022031.
PR 23-AUG-2000; 2000WO-US023522.
PR 24-AUG-2000; 2000WO-US023328.
PR 08-NOV-2000; 2000WO-US030952.
PR 01-DEC-2000; 2000WO-US032678.
PR 28-FEB-2001; 2001WO-US006520.
PR 01-JUN-2001; 2001WO-US017800.
PR 20-JUN-2001; 2001WO-US019692.
PR 29-JUN-2001; 2001WO-US021066.
PR 09-JUL-2001; 2001WO-US021735.
PR 28-AUG-2001; 2001US-00941992.
XX
PA (GETH) GENENTECH INC.
XX
PI Ashkenazi AJ, Baker KP, Botstein D, Desnoyers L, Eaton DL;
PI Ferrara N, Fong S, Gerber H, Gerritsen ME, Goddard A, Godowski PJ;
PI Grimaldi JC, Gurney AL, Kljavin IJ, Napier MA, Pan J, Paoni NF;
PI Roy MA, Stewart TA, Tumas D, Watanabe CK, Williams PM, Wood WI;
PI Zhang Z;
XX
DR WPI; 2003-352829/33.
DR P-PSDB; ABU72576.
XX
PT New genes and secreted and transmembrane polypeptides (e.g. PRO183 or
PT PRO184), useful for treating or diagnosing e.g. ovarian cancer, Kaposi's
PT sarcoma, leukemia, lymphoma, hepatitis B, multiple sclerosis or Crohn's
PT disease.
XX
PS Claim 1; Fig 299; 663pp; English.
XX
CC The invention describes a new isolated nucleic acid molecule comprising
CC the full length coding sequence of the DNA deposited with the American
CC Type Culture Collection (e.g. ATCC Deposit No. 209621, 552-PTA, 819-PTA,
CC 209439, 203135, etc); or a sequence with at least 80% identity to a DNA
CC encoding a PRO polypeptide. The PRO polypeptides or polynucleotides are
CC useful as pharmaceuticals, diagnostics, biosensors or bioreactors. These
CC are particularly useful for detecting or treating e.g. malignancies or
CC cancers (e.g. ovarian cancer, colorectal cancer, Kaposi's sarcoma,
CC leukaemia or lymphoma), hepatitis B, multiple sclerosis, or Crohn's
CC disease in mammals. The PRO polypeptides are useful in drug screening,
CC particularly as targets for therapeutic intervention in these diseases,
CC and in the diagnostic determination of the presence of these diseases.
CC The PRO polypeptides are also useful as molecular weight markers, or for
CC chromosome identification. The PRO genes are useful as hybridisation
CC probes, or for screening libraries of human cDNA, genomic DNA or mRNA.
CC The PRO genes may also be used in gene therapy, particularly for
CC replacing a defective gene. This sequence encodes a novel human secreted
CC and transmembrane PRO polypeptide
XX
SQ Sequence 1728 BP; 438 A; 360 C; 390 G; 540 T; 0 U; 0 Other;

Query Match 100.0%; Score 1728; DB 7; Length 1728;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1728; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy          1 CAGCCGGGTCCCAAGCCTGTGCCTGAGCCTGAGCCTGAGCCTGAGCCCGAGCCGGGAGCC 60
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Db          1 CAGCCGGGTCCCAAGCCTGTGCCTGAGCCTGAGCCTGAGCCTGAGCCCGAGCCGGGAGCC 60

Qy         61 GGTCGCGGGGGCTCCGGGCTGTGGGACCGCTGGGCCCCCAGCGATGGCGACCCTGTGGGG 120
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Qy        121 AGGCCTTCTTCGGCTTGGCTCCTTGCTCAGCCTGTCGTGCCTGGCGCTTTCCGTGCTGCT 180
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Db        121 AGGCCTTCTTCGGCTTGGCTCCTTGCTCAGCCTGTCGTGCCTGGCGCTTTCCGTGCTGCT 180

Qy        181 GCTGGCGCAGCTGTCAGACGCCGCCAAGAATTTCGAGGATGTCAGATGTAAATGTATCTG 240
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Qy        241 CCCTCCCTATAAAGAAAATTCTGGGCATATTTATAATAAGAACATATCTCAGAAAGATTG 300
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Qy        301 TGATTGCCTTCATGTTGTGGAGCCCATGCCTGTGCGGGGGCCTGATGTAGAAGCATACTG 360
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Qy        361 TCTACGCTGTGAATGCAAATATGAAGAAAGAAGCTCTGTCACAATCAAGGTTACCATTAT 420
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Db        361 TCTACGCTGTGAATGCAAATATGAAGAAAGAAGCTCTGTCACAATCAAGGTTACCATTAT 420

Qy        421 AATTTATCTCTCCATTTTGGGCCTTCTACTTCTGTACATGGTATATCTTACTCTGGTTGA 480
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Qy        481 GCCCATACTGAAGAGGCGCCTCTTTGGACATGCACAGTTGATACAGAGTGATGATGATAT 540
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Db        481 GCCCATACTGAAGAGGCGCCTCTTTGGACATGCACAGTTGATACAGAGTGATGATGATAT 540

Qy        541 TGGGGATCACCAGCCTTTTGCAAATGCACACGATGTGCTAGCCCGCTCCCGCAGTCGAGC 600
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Qy        601 CAACGTGCTGAACAAGGTAGAATATGCACAGCAGCGCTGGAAGCTTCAAGTCCAAGAGCA 660
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Db        601 CAACGTGCTGAACAAGGTAGAATATGCACAGCAGCGCTGGAAGCTTCAAGTCCAAGAGCA 660

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Qy        781 TTAATACCTTGTTGATTTCACCAACTGTTGCTGGAAGATTCAAAACTGGAAGCAAAAACT 840
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Qy        901 AAAGTCAGCCAATAAGTCTTTTCCTATTTGTGACTTTTACTAATAAAAATAAATCTGCCT 960
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Qy       1021 AACTTGACTTTCAAGATAATTTTCAGGGTTTTTGTTGTTGTTGTTTTTTGTTTGTTTGTT 1080
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Qy       1081 TTGGTGGGAGAGGGGAGGGATGCCTGGGAAGTGGTTAACAACTTTTTTCAAGTCACTTTA 1140
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Qy       1141 CTAAACAAACTTTTGTAAATAGACCTTACCTTCTATTTTCGAGTTTCATTTATATTTTGC 1200
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Qy       1201 AGTGTAGCCAGCCTCATCAAAGAGCTGACTTACTCATTTGACTTTTGCACTGACTGTATT 1260
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Qy       1261 ATCTGGGTATCTGCTGTGTCTGCACTTCATGGTAAACGGGATCTAAAATGCCTGGTGGCT 1320
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RESULT 12
ACA58005
ID   ACA58005 standard; cDNA; 1728 BP.
XX
AC   ACA58005;
XX
DT   09-JUN-2003  (first entry)
XX
DE   cDNA encoding human neoplasia inhibiting PRO polypeptide PRO1375.
XX
KW   Human; ss; gene; tumour; cancer; neoplasia; liver cancer; sarcoma;
KW   breast cancer; ovarian cancer; renal cancer; colorectal cancer; melanoma;
KW   uterine cancer; prostate cancer; lung cancer; bladder cancer; leukaemia;
KW   gastric cancer; pancreatic cancer; vulval cancer; thyroid cancer;
KW   central nervous system cancer; hepatic carcinoma; glioblastoma;
KW   neuronal disorder; glial disorder; astrocytal disorder;
KW   hypothalamic disorder; glandular disorder; macrophagal disorder;
KW   epithelial disorder; stromal disorder; blastocoelic disorder;
KW   inflammatory disorder; angiogenic disorder; immunologic disorder.
XX
OS   Homo sapiens.
XX
PN   US2002192209-A1.
XX
PD   19-DEC-2002.
XX
PF   30-NOV-2001; 2001US-00001054.
XX
PR   17-SEP-1997;   97US-0059114P.
PR   27-MAR-1998;   98US-0079689P.
PR   30-MAR-1998;   98US-0079920P.
PR   24-APR-1998;   98US-0082999P.
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PR   12-MAY-1998;   98US-0085149P.
PR   02-JUN-1998;   98US-0087607P.
PR   11-JUN-1998;   98US-0088858P.
PR   25-JUN-1998;   98US-0090691P.
PR   17-AUG-1998;   98US-0096891P.
PR   17-AUG-1998;   98US-0096894P.
PR   10-SEP-1998;   98US-0099803P.
PR   10-SEP-1998;   98WO-US018824.
PR   14-SEP-1998;   98US-0100263P.
PR   15-SEP-1998;   98US-0100390P.
PR   23-SEP-1998;   98US-0101476P.
PR   10-NOV-1998;   98US-0107783P.
PR   18-NOV-1998;   98US-0108849P.
PR   19-NOV-1998;   98US-00180997.
PR   15-DEC-1998;   98US-0112420P.
PR   22-DEC-1998;   98US-00218517.
PR   22-DEC-1998;   98US-0113296P.
PR   05-JAN-1999;   99WO-US000106.
PR   12-JAN-1999;   99US-0115554P.
PR   12-JAN-1999;   99US-0115558P.
PR   20-JAN-1999;   99US-0116533P.
PR   08-MAR-1999;   99WO-US005028.
PR   10-MAR-1999;   99US-0123618P.
PR   12-APR-1999;   99US-00284291.
PR   20-APR-1999;   99WO-US008615.
PR   27-APR-1999;   99US-0131294P.
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XX
PA (GETH) GENENTECH INC.
XX
PI Baker KP, Goddard A, Gurney AL, Hebert C, Henzel W, Kabakoff RC;
PI Shelton DL, Smith V, Watanabe CK, Wood WI;
XX
DR WPI; 2003-328851/06.
DR P-PSDB; ABU71431.
XX
PT Novel isolated PRO polypeptides e.g. PRO240, PRO381, PRO540, useful for
PT treating tumor, preferably cancer, or for treating neuronal, glial,
PT hypothalamic, stromal, inflammatory, angiogenic and immunologic
PT disorders.
XX
PS Claim 20; Fig 31; 186pp; English.
XX
CC The invention relates to an isolated secreted and transmembrane
CC polypeptide, designated as PRO polypeptide, PRO polypeptide lacking its
CC associated signal peptide or PRO polypeptide extracellular domain with or
CC without its associated signal peptide. The PRO polypeptide or an antibody
CC binding to it is useful for inhibiting the growth of a tumor cell. A
CC composition containing a PRO polypeptide is useful for inhibiting
CC neoplastic cell growth or for treating a tumour, preferably cancer (such
CC as liver, breast, ovarian, renal, colorectal, uterine, prostate, lung,
CC bladder, gastric, pancreatic, vulval, thyroid, central nervous system
CC cancer, hepatic carcinomas, sarcomas, glioblastomas, melanoma or
CC leukaemia) in a mammal. The PRO polypeptide is useful for identifying its
CC agonists. The PRO polypeptide or an antibody binding to it is useful in
CC the preparation of a medicament for treating a condition which is
CC responsive to the PRO polypeptide or an antibody binding to it. The PRO
CC polypeptide or an antibody binding to it is also useful for treating
CC neuronal, glial, astrocytal, hypothalamic, glandular, macrophagal,
CC epithelial, stromal, blastocoelic, inflammatory, angiogenic and
CC immunologic disorders. The present sequence represents a cDNA encoding a
CC PRO polypeptides of the invention
XX
SQ Sequence 1728 BP; 438 A; 360 C; 390 G; 540 T; 0 U; 0 Other;

Query Match 100.0%; Score 1728; DB 7; Length 1728;
Best Local Similarity 100.0%; Pred. No. 0;
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RESULT 13
ABX80895
ID   ABX80895 standard; cDNA; 1728 BP.
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AC   ABX80895;
XX
DT   22-APR-2003  (first entry)
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DE   Human secreted/transmembrane protein cDNA, #168.
XX
KW   Human; gene; ss; PRO; secreted; transmembrane; pharmaceutical;
KW   diagnostic; biosensor; bioreactor; tumour; therapeutic; gene therapy;
KW   tumour-associated antigenic target; TAT; ADEPT;
KW   antibody-dependent enzyme mediated prodrug therapy; cytostatic.
XX
OS   Homo sapiens.
XX
PN   US2003027162-A1.
XX
PD   06-FEB-2003.
XX
PF   15-NOV-2001; 2001US-00997428.
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Query Match 100.0%; Score 1728; DB 7; Length 1728;
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Db          1 CAGCCGGGTCCCAAGCCTGTGCCTGAGCCTGAGCCTGAGCCTGAGCCCGAGCCGGGAGCC 60

Qy         61 GGTCGCGGGGGCTCCGGGCTGTGGGACCGCTGGGCCCCCAGCGATGGCGACCCTGTGGGG 120
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Db         61 GGTCGCGGGGGCTCCGGGCTGTGGGACCGCTGGGCCCCCAGCGATGGCGACCCTGTGGGG 120

Qy        121 AGGCCTTCTTCGGCTTGGCTCCTTGCTCAGCCTGTCGTGCCTGGCGCTTTCCGTGCTGCT 180
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Db        121 AGGCCTTCTTCGGCTTGGCTCCTTGCTCAGCCTGTCGTGCCTGGCGCTTTCCGTGCTGCT 180

Qy        181 GCTGGCGCAGCTGTCAGACGCCGCCAAGAATTTCGAGGATGTCAGATGTAAATGTATCTG 240
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Db        181 GCTGGCGCAGCTGTCAGACGCCGCCAAGAATTTCGAGGATGTCAGATGTAAATGTATCTG 240

Qy        241 CCCTCCCTATAAAGAAAATTCTGGGCATATTTATAATAAGAACATATCTCAGAAAGATTG 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 CCCTCCCTATAAAGAAAATTCTGGGCATATTTATAATAAGAACATATCTCAGAAAGATTG 300

Qy        301 TGATTGCCTTCATGTTGTGGAGCCCATGCCTGTGCGGGGGCCTGATGTAGAAGCATACTG 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 TGATTGCCTTCATGTTGTGGAGCCCATGCCTGTGCGGGGGCCTGATGTAGAAGCATACTG 360

Qy        361 TCTACGCTGTGAATGCAAATATGAAGAAAGAAGCTCTGTCACAATCAAGGTTACCATTAT 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 TCTACGCTGTGAATGCAAATATGAAGAAAGAAGCTCTGTCACAATCAAGGTTACCATTAT 420

Qy        421 AATTTATCTCTCCATTTTGGGCCTTCTACTTCTGTACATGGTATATCTTACTCTGGTTGA 480
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Db        421 AATTTATCTCTCCATTTTGGGCCTTCTACTTCTGTACATGGTATATCTTACTCTGGTTGA 480

Qy        481 GCCCATACTGAAGAGGCGCCTCTTTGGACATGCACAGTTGATACAGAGTGATGATGATAT 540
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        481 GCCCATACTGAAGAGGCGCCTCTTTGGACATGCACAGTTGATACAGAGTGATGATGATAT 540

Qy        541 TGGGGATCACCAGCCTTTTGCAAATGCACACGATGTGCTAGCCCGCTCCCGCAGTCGAGC 600
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        541 TGGGGATCACCAGCCTTTTGCAAATGCACACGATGTGCTAGCCCGCTCCCGCAGTCGAGC 600

Qy        601 CAACGTGCTGAACAAGGTAGAATATGCACAGCAGCGCTGGAAGCTTCAAGTCCAAGAGCA 660
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Db        601 CAACGTGCTGAACAAGGTAGAATATGCACAGCAGCGCTGGAAGCTTCAAGTCCAAGAGCA 660

Qy        661 GCGAAAGTCTGTCTTTGACCGGCATGTTGTCCTCAGCTAATTGGGAATTGAATTCAAGGT 720
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Db        661 GCGAAAGTCTGTCTTTGACCGGCATGTTGTCCTCAGCTAATTGGGAATTGAATTCAAGGT 720

Qy        721 GACTAGAAAGAAACAGGCAGACAACTGGAAAGAACTGACTGGGTTTTGCTGGGTTTCATT 780
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Qy        841 TGCTTGATTTTTTTTTTCTTGTTAACGTAATAATAGAGACATTTTTAAAAGCACACAGCTC 900
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Qy        901 AAAGTCAGCCAATAAGTCTTTTCCTATTTGTGACTTTTACTAATAAAAATAAATCTGCCT 960
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Qy        961 GTAAATTATCTTGAAGTCCTTTACCTGGAACAAGCACTCTCTTTTTTCACCACATAGTTTT 1020
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Db        961 GTAAATTATCTTGAAGTCCTTTACCTGGAACAAGCACTCTCTTTTTTCACCACATAGTTTT 1020

Qy       1021 AACTTGACTTTCAAGATAATTTTCAGGGTTTTTGTTGTTGTTGTTTTTTTGTTTGTTTGTT 1080
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Db       1021 AACTTGACTTTCAAGATAATTTTCAGGGTTTTTGTTGTTGTTGTTTTTTTGTTTGTTTGTT 1080

Qy       1081 TTGGTGGGAGAGGGGAGGGATGCCTGGGAAGTGGTTAACAACTTTTTTCAAGTCACTTTA 1140
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Qy       1141 CTAAACAAACTTTTGTAAATAGACCTTACCTTCTATTTTCGAGTTTCATTTATATTTTGC 1200
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Qy       1201 AGTGTAGCCAGCCTCATCAAAGAGCTGACTTACTCATTTGACTTTTGCACTGACTGTATT 1260
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Qy       1261 ATCTGGGTATCTGCTGTGTCTGCACTTCATGGTAAACGGGATCTAAAATGCCTGGTGGCT 1320
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Db       1261 ATCTGGGTATCTGCTGTGTCTGCACTTCATGGTAAACGGGATCTAAAATGCCTGGTGGCT 1320

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Qy       1561 CGGTCGTGGTGAGAGGCAGCTGTTTGAGCTCCAATATGTGCAGCTTTGAACTAGGGCTGG 1620
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Db       1561 CGGTCGTGGTGAGAGGCAGCTGTTTGAGCTCCAATATGTGCAGCTTTGAACTAGGGCTGG 1620

Qy       1621 GGTTGTGGGTGCCTCTTCTGAAAGGTCTAACCATTATTGGATAACTGGCTTTTTTCTTCC 1680
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Qy       1681 TATGTCCTCTTTGGAATGTAACAATAAAAATAATTTTTGAAACATCAA 1728
              ||||||||||||||||||||||||||||||||||||||||||||||||
Db       1681 TATGTCCTCTTTGGAATGTAACAATAAAAATAATTTTTGAAACATCAA 1728
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RESULT 14
ACD44404
ID ACD44404 standard; cDNA; 1728 BP.
XX
AC ACD44404;
XX
DT 10-SEP-2003 (first entry)
XX
DE cDNA encoding human PRO1375 polypeptide.
XX
KW Human; PRO polypeptide; secreted protein; transmembrane protein;
KW genetic disorder; antibacterial; immunosuppressive; transgenic;
KW gene therapy; gene; ss.
XX
OS Homo sapiens.
XX
PN US2002127576-A1.
XX
PD 12-SEP-2002.
XX
PF 14-NOV-2001; 2001US-00991073.
XX
PR 16-JUN-1997; 97US-0049787P.
PR 17-OCT-1997; 97US-0062250P.
PR 05-NOV-1997; 97WO-US020069.
PR 12-NOV-1997; 97US-0065186P.
PR 13-NOV-1997; 97US-0065311P.
PR 24-NOV-1997; 97US-0066770P.
PR 25-FEB-1998; 98US-0075945P.
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PR 28-APR-1998; 98US-0083322P.
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PR 17-JUN-1998; 98US-0089653P.
PR 18-JUN-1998; 98US-0089801P.
PR 18-JUN-1998; 98US-0089907P.
PR 18-JUN-1998; 98US-0089908P.
PR 16-SEP-1998; 98WO-US019330.
PR 17-SEP-1998; 98WO-US019437.
PR 07-OCT-1998; 98WO-US021141.
PR 01-DEC-1998; 98WO-US025108.
PR 05-JAN-1999; 99WO-US000106.
PR 08-MAR-1999; 99WO-US005028.
PR 02-JUN-1999; 99WO-US012252.
PR 15-SEP-1999; 99WO-US021090.
PR 15-SEP-1999; 99WO-US021547.
PR 30-NOV-1999; 99WO-US028313.
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PR 01-DEC-1999; 99WO-US028634.
PR 16-DEC-1999; 99WO-US030095.
PR 20-DEC-1999; 99WO-US030911.
PR 06-JAN-2000; 2000WO-US000219.
PR 06-JAN-2000; 2000WO-US000376.
PR 11-FEB-2000; 2000WO-US003565.
PR 18-FEB-2000; 2000WO-US004341.
PR 22-FEB-2000; 2000WO-US004414.
PR 24-FEB-2000; 2000WO-US004914.
PR 24-FEB-2000; 2000WO-US005004.
PR 02-MAR-2000; 2000WO-US005841.
PR 10-MAR-2000; 2000WO-US006319.
PR 15-MAR-2000; 2000WO-US006884.
PR 20-MAR-2000; 2000WO-US007377.
PR 30-MAR-2000; 2000WO-US008439.
PR 15-MAY-2000; 2000WO-US013358.
PR 17-MAY-2000; 2000WO-US013705.
PR 22-MAY-2000; 2000WO-US014042.
PR 30-MAY-2000; 2000WO-US014941.
PR 02-JUN-2000; 2000WO-US015264.
PR 28-JUL-2000; 2000WO-US020710.
PR 11-AUG-2000; 2000WO-US022031.
PR 23-AUG-2000; 2000WO-US023522.
PR 24-AUG-2000; 2000WO-US023328.
PR 08-NOV-2000; 2000WO-US030952.
PR 01-DEC-2000; 2000WO-US032678.
PR 28-FEB-2001; 2001WO-US006520.
PR 01-JUN-2001; 2001WO-US017800.
PR 20-JUN-2001; 2001WO-US019692.
PR 29-JUN-2001; 2001WO-US021066.
PR 09-JUL-2001; 2001WO-US021735.
PR 28-AUG-2001; 2001US-00941992.
XX
PA (GETH) GENENTECH INC.
XX
PI Ashkenazi AJ, Baker KP, Botstein D, Desnoyers L, Eaton DL;
PI Ferrara N, Fong S, Gerber H, Gerritsen ME, Goddard A, Godowski PJ;
PI Grimaldi JC, Gurney AL, Kljavin IJ, Napier MA, Pan J, Paoni NF;
PI Roy MA, Stewart TA, Tumas D, Watanabe CK, Williams PM, Wood WI;
PI Zhang Z;
XX
DR WPI; 2003-340824/32.
DR P-PSDB; ABO26022.
XX
PT Novel isolated PRO polypeptides e.g., PRO826, PRO1068, PRO1184, PRO1346
PT and PRO1375, which stimulate proliferation of stimulated T-lymphocytes
PT and are therapeutically useful for enhancing immune responses.
XX
PS Claim 2; Fig 299; 661pp; English.

XX
CC The present invention relates to the isolation of novel human PRO
CC polypeptides, and the polynucleotide sequences encoding them. The PRO
CC polypeptides are secreted and transmembrane proteins. The PRO
CC polypeptides are useful for detecting other PRO polypeptides, for linking
CC bioactive molecules to cells expressing PRO polypeptides, for modulating
CC biological activities of cells expressing PRO polypeptides, and for for
CC identifying agonists or antagonists. The polynucleotide sequences
CC encoding PRO polypeptides are useful as hybridisation probes, in
CC chromosome and gene mapping, in the generation of antisense RNA and DNA,
CC in the preparation of PRO polypeptides, for generating transgenic animals
CC or knockout animals, to construct hybridisation probes for mapping the
CC gene which encodes the PRO polypeptide, and for the genetic analysis of
CC individuals with genetic disorders, in gene therapy, for chromosome
CC identification, as chromosome markers, and for generating probes for PCR,
CC Northern analysis, Southern analysis and Western analysis. The present
CC sequence encodes a human PRO polypeptide of the invention. Note: The
CC sequence data for this patent was obtained in electronic format directly
CC from the USPTO web site at seqdata.uspto.gov/psipsDIDEntry.html
XX
SQ Sequence 1728 BP; 438 A; 360 C; 390 G; 540 T; 0 U; 0 Other;

Query Match 100.0%; Score 1728; DB 7; Length 1728;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1728; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy    1 CAGCCGGGTCCCAAGCCTGTGCCTGAGCCTGAGCCTGAGCCTGAGCCCGAGCCGGGAGCC 60
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1 CAGCCGGGTCCCAAGCCTGTGCCTGAGCCTGAGCCTGAGCCTGAGCCCGAGCCGGGAGCC 60

Qy   61 GGTCGCGGGGGCTCCGGGCTGTGGGACCGCTGGGCCCCCAGCGATGGCGACCCTGTGGGG 120
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   61 GGTCGCGGGGGCTCCGGGCTGTGGGACCGCTGGGCCCCCAGCGATGGCGACCCTGTGGGG 120

Qy  121 AGGCCTTCTTCGGCTTGGCTCCTTGCTCAGCCTGTCGTGCCTGGCGCTTTCCGTGCTGCT 180
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Db  121 AGGCCTTCTTCGGCTTGGCTCCTTGCTCAGCCTGTCGTGCCTGGCGCTTTCCGTGCTGCT 180

Qy  181 GCTGGCGCAGCTGTCAGACGCCGCCAAGAATTTCGAGGATGTCAGATGTAAATGTATCTG 240
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Qy  241 CCCTCCCTATAAAGAAAATTCTGGGCATATTTATAATAAGAACATATCTCAGAAAGATTG 300
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Qy        721 GACTAGAAAGAAACAGGCAGACAACTGGAAAGAACTGACTGGGTTTTGCTGGGTTTCATT 780
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Qy       1081 TTGGTGGGAGAGGGGAGGGATGCCTGGGAAGTGGTTAACAACTTTTTTCAAGTCACTTTA 1140
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Db       1081 TTGGTGGGAGAGGGGAGGGATGCCTGGGAAGTGGTTAACAACTTTTTTCAAGTCACTTTA 1140

Qy       1141 CTAAACAAACTTTTGTAAATAGACCTTACCTTCTATTTTCGAGTTTCATTTATATTTTGC 1200
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Qy       1261 ATCTGGGTATCTGCTGTGTCTGCACTTCATGGTAAACGGGATCTAAAATGCCTGGTGGCT 1320
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RESULT 15
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ID ABX79575 standard; cDNA; 1728 BP.

XX
AC ABX79575;
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DT 17-APR-2003 (first entry)
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DE Human sectreted/transmembrane protein cDNA, #168.
XX
KW Human; gene; ss; PRO; secreted; transmembrane; signal peptide;
KW pharmaceutical; diagnostic; biosensor; bioreactor; tumour; therapeutic;
KW colon cancer; lung cancer; breast cancer; cancer; gene therapy.
XX
OS Homo sapiens.
XX
PN US2002142961-A1.
XX
PD 03-OCT-2002.
XX
PF 19-NOV-2001; 2001US-00989721.
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PR 16-JUN-1997; 97US-0049787P.
PR 17-OCT-1997; 97US-0062250P.
PR 05-NOV-1997; 97WO-US020069.
PR 12-NOV-1997; 97US-0065186P.
PR 13-NOV-1997; 97US-0065311P.
PR 24-NOV-1997; 97US-0066770P.
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PR 02-JUN-1998; 98US-0087607P.
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PR 03-JUN-1998; 98US-0087827P.
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PR 04-JUN-1998; 98US-0088029P.
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PR 18-JUN-1998; 98US-0089801P.
PR 18-JUN-1998; 98US-0089907P.
PR 18-JUN-1998; 98US-0089908P.
PR 16-SEP-1998; 98WO-US019330.
PR 17-SEP-1998; 98WO-US019437.
PR 07-OCT-1998; 98WO-US021141.
PR 01-DEC-1998; 98WO-US025108.

PR 05-JAN-1999; 99WO-US000106.
PR 08-MAR-1999; 99WO-US005028.
PR 02-JUN-1999; 99WO-US012252.
PR 15-SEP-1999; 99WO-US021090.
PR 15-SEP-1999; 99WO-US021547.
PR 30-NOV-1999; 99WO-US028313.
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PR 05-JAN-2000; 2000WO-US000219.
PR 06-JAN-2000; 2000WO-US000376.
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PR 22-MAY-2000; 2000WO-US014042.
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PR 02-JUN-2000; 2000WO-US015264.
PR 28-JUL-2000; 2000WO-US020710.
PR 11-AUG-2000; 2000WO-US022031.
PR 23-AUG-2000; 2000WO-US023522.
PR 24-AUG-2000; 2000WO-US023328.
PR 08-NOV-2000; 2000WO-US030952.
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PR 28-FEB-2001; 2001WO-US006520.
PR 01-JUN-2001; 2001WO-US017800.
PR 20-JUN-2001; 2001WO-US019692.
PR 29-JUN-2001; 2001WO-US021066.
PR 09-JUL-2001; 2001WO-US021735.
PR 28-AUG-2001; 2001US-00941992.
XX
PA (GETH) GENENTECH INC.
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PI Ashkenazi AJ, Baker KP, Botstein D, Desnoyers L, Eaton DL;
PI Ferrara N, Fong S, Gerber H, Gerritsen ME, Goddard A, Godowski PJ;
PI Grimaldi JC, Gurney AL, Kljavin IJ, Napier MA, Pan J, Paoni NF;
PI Roy MA, Stewart TA, Tumas D, Watanabe CK, Williams PM, Wood WI;
PI Zhang Z;
XX
DR WPI; 2003-155950/15.
DR P-PSDB; ABU59031.
XX
PT New secreted and transmembrane PRO polypeptides (e.g. PRO183, PRO184,
PT PRO361 or PRO846) useful as targets for therapeutic intervention in
PT cancers (e.g. lung or breast cancers), or for diagnosing these cancers.
XX
PS Claim 2; Fig 299; 647pp; English.
XX
CC The invention discloses isolated PRO secreted/transmembrane polypeptides
CC comprising a sequence without signal peptide and the nucleic acid
CC encoding them. The polypeptides can be used to raise antibodies that
CC specifically bind to the PRO polypeptide, for linking a bioactive
CC molecule to a cell expressing a PRO protein and for modulating at least
CC one biological activity of a cell. The PRO polypeptides or
CC polynucleotides are also useful as pharmaceuticals, diagnostics,
CC biosensors or bioreactors, for detecting or treating e.g. tumours in
CC mammals, e.g. humans, dogs, cats, cattle, horses, sheep, pigs, goats or
CC rabbits as targets for therapeutic intervention in certain cancers (e.g.
CC colon, lung or breast cancers) and diagnostic determination of the
CC presence of these cancers. The PRO polypeptides are also useful as
CC molecular weight markers or for chromosome identification. The PRO genes
CC are useful as hybridisation probes or for screening libraries of human
CC cDNA, genomic DNA or mRNA. The PRO genes may also be used in gene
CC therapy, particularly for replacing a defective gene. The sequences
CC presented in ABX79290-ABX79675 are the genes encoding, the primers
CC amplifying and the probes detecting the PRO polynucleotides of the
CC invention. Note: The sequence data for this patent is also available in
CC electronic format from USPTO at seqdata.uspto.gov/sequence.html
XX
SQ Sequence 1728 BP; 438 A; 360 C; 390 G; 540 T; 0 U; 0 Other;

Query Match 100.0%; Score 1728; DB 7; Length 1728;
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Matches 1728; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy        121 AGGCCTTCTTCGGCTTGGCTCCTTGCTCAGCCTGTCGTGCCTGGCGCTTTCCGTGCTGCT 180
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Qy        181 GCTGGCGCAGCTGTCAGACGCCGCCAAGAATTTCGAGGATGTCAGATGTAAATGTATCTG 240
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Qy        241 CCCTCCCTATAAAGAAAATTCTGGGCATATTTATAATAAGAACATATCTCAGAAAGATTG 300
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Qy        301 TGATTGCCTTCATGTTGTGGAGCCCATGCCTGTGCGGGGGCCTGATGTAGAAGCATACTG 360
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Qy       1021 AACTTGACTTTCAAGATAATTTTCAGGGTTTTTGTTGTTGTTGTTTTTTGTTTGTTTGTT 1080
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Qy       1081 TTGGTGGGAGAGGGGAGGGATGCCTGGGAAGTGGTTAACAACTTTTTTCAAGTCACTTTA 1140
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Job time : 699 secs

GenCore version 5.1.6

OM nucleic - nucleic search, using sw model

Run on: April 20, 2004, 01:58:41 ; Search time 6718 Seconds
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Title: US-09-989-725-417
Perfect score: 1728
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Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 3470272 seqs, 21671516995 residues

Total number of hits satisfying chosen parameters: 6940544

Minimum DB seq length: 0
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Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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7		1690.4	97.8	1772	9	BC040124	BC040124 Homo sapi
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38	c	280.6	16.2	437	11	G21187	G21187 human STS W
39	c	279.4	16.2	207364	2	AC120564	AC120564 Rattus no
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ALIGNMENTS

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DEFINITION Sequence 417 from patent US 6478825.
ACCESSION AR252653
VERSION AR252653.1 GI:27300561
KEYWORDS .
SOURCE Unknown.
ORGANISM Unknown.
Unclassified.
REFERENCE 1 (bases 1 to 1728)
AUTHORS Winterbottom,J.M., Shimp,L., Boyce,T.M. and Kaes,D.
TITLE Implant, method of making same and use of the implant for the treatment of bone defects
JOURNAL Patent: US 6478825-A 417 12-NOV-2002;

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                     /mol_type="genomic DNA"
ORIGIN

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Qy          1 CAGCCGGGTCCCAAGCCTGTGCCTGAGCCTGAGCCTGAGCCTGAGCCCGAGCCGGGAGCC 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 CAGCCGGGTCCCAAGCCTGTGCCTGAGCCTGAGCCTGAGCCTGAGCCCGAGCCGGGAGCC 60

Qy         61 GGTCGCGGGGGCTCCGGGCTGTGGGACCGCTGGGCCCCCAGCGATGGCGACCCTGTGGGG 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 GGTCGCGGGGGCTCCGGGCTGTGGGACCGCTGGGCCCCCAGCGATGGCGACCCTGTGGGG 120

Qy        121 AGGCCTTCTTCGGCTTGGCTCCTTGCTCAGCCTGTCGTGCCTGGCGCTTTCCGTGCTGCT 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 AGGCCTTCTTCGGCTTGGCTCCTTGCTCAGCCTGTCGTGCCTGGCGCTTTCCGTGCTGCT 180

Qy        181 GCTGGCGCAGCTGTCAGACGCCGCCAAGAATTTCGAGGATGTCAGATGTAAATGTATCTG 240
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Qy        241 CCCTCCCTATAAAGAAAATTCTGGGCATATTTATAATAAGAACATATCTCAGAAAGATTG 300
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Db        301 TGATTGCCTTCATGTTGTGGAGCCCATGCCTGTGCGGGGGCCTGATGTAGAAGCATACTG 360

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Db        361 TCTACGCTGTGAATGCAAATATGAAGAAAGAAGCTCTGTCACAATCAAGGTTACCATTAT 420

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Qy        601 CAACGTGCTGAACAAGGTAGAATATGCACAGCAGCGCTGGAAGCTTCAAGTCCAAGAGCA 660
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Qy        721 GACTAGAAAGAAACAGGCAGACAACTGGAAAGAACTGACTGGGTTTTGCTGGGTTTCATT 780
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Qy        781 TTAATACCTTGTTGATTTCACCAACTGTTGCTGGAAGATTCAAAACTGGAAGCAAAAACT 840
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Qy       1021 AACTTGACTTTCAAGATAATTTTCAGGGTTTTTGTTGTTGTTGTTTTTTGTTTGTTTGTT 1080
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Qy       1081 TTGGTGGGAGAGGGGAGGGATGCCTGGGAAGTGGTTAACAACTTTTTTCAAGTCACTTTA 1140
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Qy       1141 CTAAACAAACTTTTGTAAATAGACCTTACCTTCTATTTTCGAGTTTCATTTATATTTTGC 1200
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Qy       1201 AGTGTAGCCAGCCTCATCAAAGAGCTGACTTACTCATTTGACTTTTGCACTGACTGTATT 1260
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Db       1201 AGTGTAGCCAGCCTCATCAAAGAGCTGACTTACTCATTTGACTTTTGCACTGACTGTATT 1260

Qy       1261 ATCTGGGTATCTGCTGTGTCTGCACTTCATGGTAAACGGGATCTAAAATGCCTGGTGGCT 1320
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Qy       1321 TTTCACAAAAAGCAGATTTTCTTCATGTACTGTGATGTCTGATGCAATGCATCCTAGAAC 1380
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Qy       1381 AAACTGGCCATTTGCTAGTTTACTCTAAAGACTAAACATAGTCTTGGTGTGTGTGGTCTT 1440
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Qy       1501 ATTTTATTTTAAACCCAAGCCTCCCTGGATTGATAATATATACACATTTGTCAGCATTTC 1560
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Qy       1561 CGGTCGTGGTGAGAGGCAGCTGTTTGAGCTCCAATATGTGCAGCTTTGAACTAGGGCTGG 1620
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Db       1621 GGTTGTGGGTGCCTCTTCTGAAAGGTCTAACCATTATTGGATAACTGGCTTTTTTCTTCC 1680

Qy       1681 TATGTCCTCTTTGGAATGTAACAATAAAAATAATTTTTGAAACATCAA 1728
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RESULT 2
AX055468
LOCUS       AX055468               1728 bp    DNA     linear   PAT 13-JAN-2001
DEFINITION  Sequence 98 from Patent WO0073452.
ACCESSION   AX055468
VERSION     AX055468.1  GI:12228731
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
  AUTHORS   Ashkenazi,A.J., Baker,K.P., Chan,B., Goddard,A., Godowski,P.J.,
            Gurney,A.L., Hebert,C., Henzel,W., Kabakoff,R.C., Shelton,D.L.,
            Tumas,D., Watanabe,C.K. and Wood,W.I.
  TITLE     Compositions and methods for the treatment of immune related
            diseases
  JOURNAL   Patent: WO 0073452-A 98 07-DEC-2000;
            Genentech, Inc. (US)
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                     /mol_type="unassigned DNA"
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ORIGIN

  Query Match             100.0%;  Score 1728;  DB 6;  Length 1728;
  Best Local Similarity   100.0%;  Pred. No. 0;
  Matches 1728;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 CAGCCGGGTCCCAAGCCTGTGCCTGAGCCTGAGCCTGAGCCTGAGCCCGAGCCGGGAGCC 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 CAGCCGGGTCCCAAGCCTGTGCCTGAGCCTGAGCCTGAGCCTGAGCCCGAGCCGGGAGCC 60

Qy         61 GGTCGCGGGGGCTCCGGGCTGTGGGACCGCTGGGCCCCCAGCGATGGCGACCCTGTGGGG 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 GGTCGCGGGGGCTCCGGGCTGTGGGACCGCTGGGCCCCCAGCGATGGCGACCCTGTGGGG 120

Qy        121 AGGCCTTCTTCGGCTTGGCTCCTTGCTCAGCCTGTCGTGCCTGGCGCTTTCCGTGCTGCT 180
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Db        121 AGGCCTTCTTCGGCTTGGCTCCTTGCTCAGCCTGTCGTGCCTGGCGCTTTCCGTGCTGCT 180

Qy        181 GCTGGCGCAGCTGTCAGACGCCGCCAAGAATTTCGAGGATGTCAGATGTAAATGTATCTG 240
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Qy        241 CCCTCCCTATAAAGAAAATTCTGGGCATATTTATAATAAGAACATATCTCAGAAAGATTG 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Qy        601 CAACGTGCTGAACAAGGTAGAATATGCACAGCAGCGCTGGAAGCTTCAAGTCCAAGAGCA 660
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RESULT 3
AX055716
LOCUS       AX055716                1728 bp    DNA     linear   PAT 13-JAN-2001
DEFINITION  Sequence 31 from Patent WO0073348.
ACCESSION   AX055716
VERSION     AX055716.1  GI:12228841
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
  AUTHORS   Baker,K.P., Goddard,A., Gurney,A.L., Hebert,C., Henzel,W.,
            Kabakoff,R.C., Shelton,D.L., Smith,V., Watanabe,C.K. and Wood,W.I.
  TITLE     Methods and compositions for inhibiting neoplastic cell growth
  JOURNAL   Patent: WO 0073348-A 31 07-DEC-2000;
            Genentech, Inc. (US)
FEATURES             Location/Qualifiers
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ORIGIN

  Query Match           100.0%;  Score 1728;  DB 6;  Length 1728;
  Best Local Similarity  100.0%;  Pred. No. 0;
  Matches 1728;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 CAGCCGGGTCCCAAGCCTGTGCCTGAGCCTGAGCCTGAGCCTGAGCCCGAGCCGGGAGCC 60
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Qy        301 TGATTGCCTTCATGTTGTGGAGCCCATGCCTGTGCGGGGGCCTGATGTAGAAGCATACTG 360
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Qy        721 GACTAGAAAGAAACAGGCAGACAACTGGAAAGAACTGACTGGGTTTTGCTGGGTTTCATT 780
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Qy       1141 CTAAACAAACTTTTGTAAATAGACCTTACCTTCTATTTTCGAGTTTCATTTATATTTTGC 1200
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Qy       1261 ATCTGGGTATCTGCTGTGTCTGCACTTCATGGTAAACGGGATCTAAAATGCCTGGTGGCT 1320
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Qy       1681 TATGTCCTCTTTGGAATGTAACAATAAAAATAATTTTTGAAACATCAA 1728
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Db       1681 TATGTCCTCTTTGGAATGTAACAATAAAAATAATTTTTGAAACATCAA 1728


RESULT 4
AX077037
LOCUS       AX077037               1728 bp    DNA     linear   PAT 22-FEB-2001
DEFINITION  Sequence 25 from Patent WO0105972.
ACCESSION   AX077037
VERSION     AX077037.1  GI:13121664
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
  AUTHORS   Ashkenazi,A.J., Baker,K.P., Fong,S., Goddard,A., Godowski,P.J.,
            Gurney,A.L., Hillan,K.J., Mark,M.R., Marsters,S.A., Pitti,R.M.,
            Tumas,D., Watanabe,C.K. and Wood,W.I.
  TITLE     Compositions and methods for the treatment of immune related
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  JOURNAL   Patent: WO 0105972-A 25 25-JAN-2001;
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FEATURES             Location/Qualifiers
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ORIGIN

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  Best Local Similarity  100.0%;  Pred. No. 0;
  Matches 1728;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 CAGCCGGGTCCCAAGCCTGTGCCTGAGCCTGAGCCTGAGCCTGAGCCCGAGCCGGGAGCC 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 CAGCCGGGTCCCAAGCCTGTGCCTGAGCCTGAGCCTGAGCCCGAGCCGGGAGCC 60

Qy         61 GGTCGCGGGGGCTCCGGGCTGTGGGACCGCTGGGCCCCCAGCGATGGCGACCCTGTGGGG 120
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Db         61 GGTCGCGGGGGCTCCGGGCTGTGGGACCGCTGGGCCCCCAGCGATGGCGACCCTGTGGGG 120

Qy        121 AGGCCTTCTTCGGCTTGGCTCCTTGCTCAGCCTGTCGTGCCTGGCGCTTTCCGTGCTGCT 180
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Db        121 AGGCCTTCTTCGGCTTGGCTCCTTGCTCAGCCTGTCGTGCCTGGCGCTTTCCGTGCTGCT 180

Qy        181 GCTGGCGCAGCTGTCAGACGCCGCCAAGAATTTCGAGGATGTCAGATGTAAATGTATCTG 240
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RESULT 5
AX403530
LOCUS       AX403530               1728 bp    DNA     linear   PAT 14-JUN-2002
DEFINITION  Sequence 417 from Patent WO0073454.
ACCESSION   AX403530
VERSION     AX403530.1  GI:21437007
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
  AUTHORS   Ashkenazi,A.J., Baker,K.P., Botstein,D., Desnoyers,L., Eaton,D.,
            Ferrara,N., Gerber,H., Gerritsen,M., Goddard,A., Godowski,P.,
            Grimaldi,C.J., Gurney,A.L., Kljavin,I., Napier,M.A., Pan,J.,
            Paoni,N.F., Roy,M., Stewart,T.A., Tumas,D., Watanabe,C.K.,
            Williams,P., Wood,W.I. and Zhang,Z.
  TITLE     Secreted and transmembrane polypeptides and nucleic acids encoding
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  JOURNAL   Patent: WO 0073454-A 417 07-DEC-2000;
            Genentech Inc. (US)
FEATURES             Location/Qualifiers
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ORIGIN

  Query Match           100.0%;  Score 1728;  DB 6;  Length 1728;
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Qy       1381 AAACTGGCCATTTGCTAGTTTACTCTAAAGACTAAACATAGTCTTGGTGTGTGTGGTCTT 1440
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Qy       1561 CGGTCGTGGTGAGAGGCAGCTGTTTGAGCTCCAATATGTGCAGCTTTGAACTAGGGCTGG 1620
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RESULT 6
AY359069
LOCUS       AY359069                1728 bp    mRNA    linear   PRI 03-OCT-2003
DEFINITION  Homo sapiens clone DNA67004 C11orf15 (UNQ712) mRNA, complete cds.
ACCESSION   AY359069
VERSION     AY359069.1  GI:37183255
KEYWORDS    FLI_CDNA.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 1728)
  AUTHORS   Clark,H.F., Gurney,A.L., Abaya,E., Baker,K., Baldwin,D., Brush,J.,
            Chen,J., Chow,B., Chui,C., Crowley,C., Currell,B., Deuel,B.,
            Dowd,P., Eaton,D., Foster,J., Grimaldi,C., Gu,Q., Hass,P.E.,
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            Heldens,S., Huang,A., Kim,H.S., Klimowski,L., Jin,Y., Johnson,S.,
            Lee,J., Lewis,L., Liao,D., Mark,M., Robbie,E., Sanchez,C.,
            Schoenfeld,J., Seshagiri,S., Simmons,L., Singh,J., Smith,V.,
            Stinson,J., Vagts,A., Vandlen,R., Watanabe,C., Wieand,D., Woods,K.,
            Xie,M.H., Yansura,D., Yi,S., Yu,G., Yuan,J., Zhang,M., Zhang,Z.,
            Goddard,A., Wood,W.I. and Godowski,P.
  TITLE     The Secreted Protein Discovery Initiative (SPDI), a Large-Scale
            Effort to Identify Novel Human Secreted and Transmembrane Proteins:
            A Bioinformatics Assessment
  JOURNAL   Genome Res. 13 (10), 2265-2270 (2003)
   PUBMED   12975309
REFERENCE   2  (bases 1 to 1728)
  AUTHORS   Clark,H.F.
  TITLE     Direct Submission
  JOURNAL   Submitted (01-AUG-2003) Department of Bioinformatics, Genentech,
            Inc., 1 DNA Way, South San Francisco, CA 94080, USA
FEATURES             Location/Qualifiers
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                     /clone="DNA67004"
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     CDS             104. .700
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                     /note="PRO1375"
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                     /db_xref="GI:37183256"
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                     ICPPYKENSGHIYNKNISQKDCDCLHVVEPMPVRGPDVEAYCLRCECKYEERSSVTIK
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                     RSRSRANVLNKVEYAQQRWKLQVQEQRKSVFDRHVVLS"
ORIGIN

  Query Match           100.0%;  Score 1728;  DB 9;  Length 1728;
  Best Local Similarity  100.0%;  Pred. No. 0;
  Matches 1728;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 CAGCCGGGTCCCAAGCCTGTGCCTGAGCCTGAGCCTGAGCCTGAGCCCGAGCCGGGAGCC 60
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Db          1 CAGCCGGGTCCCAAGCCTGTGCCTGAGCCTGAGCCTGAGCCTGAGCCCGAGCCGGGAGCC 60

Qy         61 GGTCGCGGGGGCTCCGGGCTGTGGGACCGCTGGGCCCCCAGCGATGGCGACCCTGTGGGG 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 GGTCGCGGGGGCTCCGGGCTGTGGGACCGCTGGGCCCCCAGCGATGGCGACCCTGTGGGG 120

Qy        121 AGGCCTTCTTCGGCTTGGCTCCTTGCTCAGCCTGTCGTGCCTGGCGCTTTCCGTGCTGCT 180
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Qy        181 GCTGGCGCAGCTGTCAGACGCCGCCAAGAATTTCGAGGATGTCAGATGTAAATGTATCTG 240
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Qy        241 CCCTCCCTATAAAGAAAATTCTGGGCATATTTATAATAAGAACATATCTCAGAAAGATTG 300
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Qy        301 TGATTGCCTTCATGTTGTGGAGCCCATGCCTGTGCGGGGGCCTGATGTAGAAGCATACTG 360
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Db        301 TGATTGCCTTCATGTTGTGGAGCCCATGCCTGTGCGGGGGCCTGATGTAGAAGCATACTG 360

Qy        361 TCTACGCTGTGAATGCAAATATGAAGAAAGAAGCTCTGTCACAATCAAGGTTACCATTAT 420
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Qy        421 AATTTATCTCTCCATTTTGGGCCTTCTACTTCTGTACATGGTATATCTTACTCTGGTTGA 480
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Db        421 AATTTATCTCTCCATTTTGGGCCTTCTACTTCTGTACATGGTATATCTTACTCTGGTTGA 480

Qy        481 GCCCATACTGAAGAGGCGCCTCTTTGGACATGCACAGTTGATACAGAGTGATGATGATAT 540
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Db        481 GCCCATACTGAAGAGGCGCCTCTTTGGACATGCACAGTTGATACAGAGTGATGATGATAT 540

Qy        541 TGGGGATCACCAGCCTTTTGCAAATGCACACGATGTGCTAGCCCGCTCCCGCAGTCGAGC 600
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Db        541 TGGGGATCACCAGCCTTTTGCAAATGCACACGATGTGCTAGCCCGCTCCCGCAGTCGAGC 600

Qy        601 CAACGTGCTGAACAAGGTAGAATATGCACAGCAGCGCTGGAAGCTTCAAGTCCAAGAGCA 660
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Qy        661 GCGAAAGTCTGTCTTTGACCGGCATGTTGTCCTCAGCTAATTGGGAATTGAATTCAAGGT 720
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        661 GCGAAAGTCTGTCTTTGACCGGCATGTTGTCCTCAGCTAATTGGGAATTGAATTCAAGGT 720

Qy        721 GACTAGAAAGAAACAGGCAGACAACTGGAAAGAACTGACTGGGTTTTGCTGGGTTTCATT 780
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Db        721 GACTAGAAAGAAACAGGCAGACAACTGGAAAGAACTGACTGGGTTTTGCTGGGTTTCATT 780

Qy        781 TTAATACCTTGTTGATTTCACCAACTGTTGCTGGAAGATTCAAAACTGGAAGCAAAAACT 840
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Db        781 TTAATACCTTGTTGATTTCACCAACTGTTGCTGGAAGATTCAAAACTGGAAGCAAAAACT 840

Qy        841 TGCTTGATTTTTTTTTCTTGTTAACGTAATAATAGAGACATTTTTAAAAGCACACAGCTC 900
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Qy        901 AAAGTCAGCCAATAAGTCTTTTCCTATTTGTGACTTTTACTAATAAAAATAAATCTGCCT 960
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        901 AAAGTCAGCCAATAAGTCTTTTCCTATTTGTGACTTTTACTAATAAAAATAAATCTGCCT 960

Qy        961 GTAAATTATCTTGAAGTCCTTTACCTGGAACAAGCACTCTCTTTTTCACCACATAGTTTT 1020
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Db        961 GTAAATTATCTTGAAGTCCTTTACCTGGAACAAGCACTCTCTTTTTCACCACATAGTTTT 1020

Qy       1021 AACTTGACTTTCAAGATAATTTTCAGGGTTTTTGTTGTTGTTGTTTTTTGTTTGTTTGTT 1080
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Qy       1201 AGTGTAGCCAGCCTCATCAAAGAGCTGACTTACTCATTTGACTTTTGCACTGACTGTATT 1260
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Qy       1261 ATCTGGGTATCTGCTGTGTCTGCACTTCATGGTAAACGGGATCTAAAATGCCTGGTGGCT 1320
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RESULT 7
BC040124
LOCUS       BC040124                1772 bp    mRNA    linear   PRI 07-OCT-2003
DEFINITION  Homo sapiens chromosome 11 open reading frame 15, mRNA (cDNA clone
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ACCESSION   BC040124
VERSION     BC040124.1  GI:25304014
KEYWORDS    MGC.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 1772)
  AUTHORS   Strausberg,R.L., Feingold,E.A., Grouse,L.H., Derge,J.G.,
            Klausner,R.D., Collins,F.S., Wagner,L., Shenmen,C.M., Schuler,G.D.,
            Altschul,S.F., Zeeberg,B., Buetow,K.H., Schaefer,C.F., Bhat,N.K.,
            Hopkins,R.F., Jordan,H., Moore,T., Max,S.I., Wang,J., Hsieh,F.,
            Diatchenko,L., Marusina,K., Farmer,A.A., Rubin,G.M., Hong,L.,
            Stapleton,M., Soares,M.B., Bonaldo,M.F., Casavant,T.L.,
            Scheetz,T.E., Brownstein,M.J., Usdin,T.B., Toshiyuki,S.,
            Carninci,P., Prange,C., Raha,S.S., Loquellano,N.A., Peters,G.J.,
            Abramson,R.D., Mullahy,S.J., Bosak,S.A., McEwan,P.J.,
            McKernan,K.J., Malek,J.A., Gunaratne,P.H., Richards,S.,
            Worley,K.C., Hale,S., Garcia,A.M., Gay,L.J., Hulyk,S.W.,
            Villalon,D.K., Muzny,D.M., Sodergren,E.J., Lu,X., Gibbs,R.A.,
            Fahey,J., Helton,E., Ketteman,M., Madan,A., Rodrigues,S.,
            Sanchez,A., Whiting,M., Madan,A., Young,A.C., Shevchenko,Y.,
            Bouffard,G.G., Blakesley,R.W., Touchman,J.W., Green,E.D.,
            Dickson,M.C., Rodriguez,A.C., Grimwood,J., Schmutz,J., Myers,R.M.,
            Butterfield,Y.S., Krzywinski,M.I., Skalska,U., Smailus,D.E.,
            Schnerch,A., Schein,J.E., Jones,S.J. and Marra,M.A.
  TITLE     Generation and initial analysis of more than 15,000 full-length
            human and mouse cDNA sequences
  JOURNAL   Proc. Natl. Acad. Sci. U.S.A. 99 (26), 16899-16903 (2002)
  MEDLINE   22388257
   PUBMED   12477932
REFERENCE   2  (bases 1 to 1772)
  AUTHORS   Strausberg,R.
  TITLE     Direct Submission
  JOURNAL   Submitted (22-NOV-2002) National Institutes of Health, Mammalian
            Gene Collection (MGC), Cancer Genomics Office, National Cancer
            Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
            USA
  REMARK    NIH-MGC Project URL: http://mgc.nci.nih.gov
COMMENT     Contact: MGC help desk
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: ATCC
            cDNA Library Preparation: Life Technologies, Inc.
            cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
            DNA Sequencing by: Institute for Systems Biology
            http://www.systemsbiology.org
            contact: amadan@systemsbiology.org
            Anup Madan, Jessica Fahey, Erin Helton, Mark Ketteman, Anuradha
            Madan, Stephanie Rodrigues, Amy Sanchez and Michelle Whiting

            Clone distribution: MGC clone distribution information can be found
            through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov
            Series: IRAK Plate: 84 Row: o Column: 11
            This clone was selected for full length sequencing because it
            passed the following selection criteria: matched mRNA gi: 11034854.
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ORIGIN

  Query Match             97.8%;  Score 1690.4;  DB 9;  Length 1772;
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  Matches 1719;  Conservative    0;  Mismatches    1;  Indels    8;  Gaps    2;

Qy          1 CAGCCGGGTCCCAAGCCTGTGCCTGAGCCTGAGCCTGAGCCTGAGCCCGAGCCGGGAGCC 60
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Db         40 CAGCCGGGTCCCAAGCCTGTGCCTGAGCCTGAGCCTGAGCCTGAGCCCGAGCCGGGAGCC 99

Qy         61 GGTCGCGGGGGGCTCCGGGCTGTGGGACCGCTGGGCCCCCAGCGATGGCGACCCTGTGGGG 120
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Db        100 GGTCGCGGGGGCTCCGGGCTGTGGGACCGCTGGGCCCCCAGCGATGGCGACCCTGTGGGG 159

Qy        121 AGGCCTTCTTCGGCTTGGCTCCTTGCTCAGCCTGTCGTGCCTGGCGCTTTCCGTGCTGCT 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Qy        181 GCTGGCGCAGCTGTCAGACGCCGCCAAGAATTTCGAGGATGTCAGATGTAAATGTATCTG 240
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Qy        241 CCCTCCCTATAAAGAAAATTCTGGGCATATTTATAATAAGAACATATCTCAGAAAGATTG 300
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Qy        301 TGATTGCCTTCATGTTGTGGAGCCCATGCCTGTGCGGGGGCCTGATGTAGAAGCATACTG 360
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Qy        361 TCTACGCTGTGAATGCAAATATGAAGAAAGAAGCTCTGTCACAATCAAGGTTACCATTAT 420
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Qy        421 AATTTATCTCTCCATTTTGGGCCTTCTACTTCTGTACATGGTATATCTTACTCTGGTTGA 480
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Qy        481 GCCCATACTGAAGAGGCGCCTCTTTGGACATGCACAGTTGATACAGAGTGATGATGATAT 540
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Qy        541 TGGGGATCACCAGCCTTTTGCAAATGCACACGATGTGCTAGCCCGCTCCCGCAGTCGAGC 600
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Qy        781 TTAATACCTTGTTGATTTCACCAACTGTTGCTGGAAGATTCAAAACTGGAAGCAAAAACT 840
Db        820 TTAATACCTTGTTGATTTCACCAACTGTTGCTGGAAGATTCAAAACTGGAAGCAAAAACT 879
Qy        841 TGCTTGATTTTTTTTTCTTGTTAACGTAATAATAGAGACATTTTTAAAAGCACACAGCTC 900
Db        880 TGCTTGA-TTTTTTTTCTTGTTAACGTAATAATAGAGACATTTTTAAAAGCACACAGCTC 938
Qy        901 AAAGTCAGCCAATAAGTCTTTTCCTATTTGTGACTTTTACTAATAAAAATAAATCTGCCT 960
Db        939 AAAGTCAGCCAATAAGTCTTTTCCTATTTGTGACTTTTACTAATAAAAATAAATCTGCCT 998
Qy        961 GTAAATTATCTTGAAGTCCTTTACCTGGAACAAGCACTCTCTTTTTCACCACATAGTTTT 1020
Db        999 GTAAATTATCTTGAAGTCCTTTACCTGGAACAAGCACTCTCTTTTTCACCACATAGTTTT 1058
Qy       1021 AACTTGACTTTCAAGATAATTTTCAGGGTTTTTGTTGTTGTTGTTTTTTGTTTGTTTGTT 1080
Db       1059 AACTTGACTTTCAAGATAATTTTCAGGGTTTTTGTTGTTGTTGTTTTTTGTTTGTTTGTT 1118
Qy       1081 TTGGTGGGAGAGGGGAGGGATGCCTGGGAAGTGGTTAACAACTTTTTTCAAGTCACTTTA 1140
Db       1119 TTGGTGGGAGAGGGGAGGGATGCCTGGGAAGTGGTTAACAACTTTTTTCAAGTCACTTTA 1178
Qy       1141 CTAAACAAACTTTTGTAAATAGACCTTACCTTCTATTTTCGAGTTTCATTTATATTTTGC 1200
Db       1179 CTAAACAAACTTTTGTAAATAGACCTTACCTTCTATTTTCGAGTTTCATTTATATTTTGC 1238
Qy       1201 AGTGTAGCCAGCCTCATCAAAGAGCTGACTTACTCATTTGACTTTTGCACTGACTGTATT 1260
Db       1239 AGTGTAGCCAGCCTCATCAAAGAGCTGACTTACTCATTTGACTTTTGCACTGACTGTATT 1298
Qy       1261 ATCTGGGTATCTGCTGTGTCTGCACTTCATGGTAAACGGGATCTAAAATGCCTGGTGGCT 1320
Db       1299 ATCTGGGTATCTGCTGTGTCTGCACTTCATGGTAAACGGGATCTAAAATGCCTGGTGGCT 1358
Qy       1321 TTTCACAAAAAGCAGATTTTCTTCATGTACTGTGATGTCTGATGCAATGCATCCTAGAAC 1380
Db       1359 TTTCACAAAAAGCAGATTTTCTTCATGTACTGTGATGTCTGATGCAATGCATCCTAGAAC 1418
Qy       1381 AAACTGGCCATTTGCTAGTTTACTCTAAAGACTAAACATAGTCTTGGTGTGTGTGGTCTT 1440
Db       1419 AAACTGGCCATTTGCTAGTTTACTCTAAAGACTAAACATAGTCTTGGTGTGTGTGGTCTT 1478
Qy       1441 ACTCATCTTCTAGTACCTTTAAGGACAAATCCTAAGGACTTGGACACTTGCAATAAAGAA 1500
Db       1479 ACTCATCTTCTAGTACCTTTAAGGACAAATCCTAAGGACTTGGACACTTGCAATAAAGAA 1538
Qy       1501 ATTTTATTTTAAACCCAAGCCTCCCTGGATTGATAATATATACACATTTGTCAGCATTTC 1560
Db       1539 ATTTTATTTTAAACCCAAGCCTCCCTGGATTGATAATATATACACATTTGTCAGCATTTC 1598
Qy       1561 CGGTCGTGGTGAGAGGCAGCTGTTTGAGCTCCAATATGTGCAGCTTTGAACTAGGGCTGG 1620
Db       1599 CGGTCGTGGTGAGAGGCAGCTGTTTGAGCTCCAATGTGTGCAGCTTTGAACTAGGGCTGG 1658
Qy       1621 GGTTGTGGGTGCCTCTTCTGAAAGGTCTAACCATTATTGGATAACTGGCTTTTTTCTTCC 1680
Db       1659 GGTTGTGGGTGCCTCTTCTGAAAGGTCTAACCATTATTGGATAACTGGCTTTTTTCT--- 1715
Qy       1681 TATGTCCTCTTTGGAATGTAACAATAAAAATAATTTTTGAAACATCAA 1728
Db       1716 ----TCCTCTTTGGAATGTAACAATAAAAATAATTTTTGAAACATCAA 1759

RESULT 8
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BD222662
LOCUS       BD222662                1834 bp    DNA     linear   PAT 17-JUL-2003
DEFINITION  Human signal peptide-containing protein.
ACCESSION   BD222662
VERSION     BD222662.1  GI:33032432
KEYWORDS    JP 2002519030-A/8.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 1834)
  AUTHORS   Lal,P., Tang,Y.T., Gorgone,G.A., Corley,N.C., Guegler,K.J.,
            Baughn,M.R., Akerblom,I.E., Young,J.A., Yue,H., Patterson,C.,
            Reddy,R., Hillman,J.L. and Bandman,O.
  TITLE     Human signal peptide-containing protein
  JOURNAL   Patent: JP 2002519030-A 8 02-JUL-2002;
            INCYTE PHARMACEUTICALS INC
COMMENT     OS   Homo sapiens (human)
            PN   JP 2002519030-A/8
            PD   02-JUL-2002
            PF   25-JUN-1999 JP 2000557363
            PR   26-JUN-1998 US    60/090762,31-JUL-1998 US    60/094983 PR
            01-OCT-1998 US    60/102686,11-DEC-1998 US    60/112129 PI   PREETI
            LAL,Y TOM TANG,GINA A GORGONE,NEIL C CORLEY,KARL J  PI   GUEGLER,
            PI   MARIAH R BAUGHN,INGRID E AKERBLOM,JANICE AU YOUNG,HENRY YUE,
            PI   CHANDRA PATTERSON,ROOPA REDDY,JENNIFER L HILLMAN,OLGA BANDMAN
            PC   C12N15/09,A61K38/00,A61K39/395,A61K45/00,A61P9/00,A61P15/00,
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            PC   A61P29/00,A61P35/00,A61P43/00,C07K14/47,C07K16/18,C12N1/15, PC
             C12N1/19,
            PC   C12N1/21,C12N5/10,C12P21/02,C12Q1/68,G01N33/68//C12P21/08, PC
             C12N15/00,
            PC   A61K37/02,C12N5/00
            CC   Incyte Clone No: 1259405
            FH   Key             Location/Qualifiers
            FT   source          1. .1834
            FT                   /organism='Homo sapiens (human)'.
FEATURES             Location/Qualifiers
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ORIGIN

  Query Match           97.5%;  Score 1685.4;  DB 6;  Length 1834;
  Best Local Similarity  99.2%;  Pred. No. 0;
  Matches 1706;  Conservative    0;  Mismatches    6;  Indels    7;  Gaps    1;

Qy         10 CCCAAGCCTGTGCCTGAGCCTGAGCCTGAGCCTGAGCCCGAGCCGGGAGCCGGTCGCGGG 69
Db         41 CCTGTGCCTGTGCCTGAGCCTGAGCCTGAGCCTGAGCCCGAGCCGGGAGCCGGTCGCGGG 100
Qy         70 GGCTCCGGGCTGTGGGACCGCTGGGCCCCCAGCGATGGCGACCCTGTGGGGAGGCCTTCT 129
Db        101 GGCTCCGGGCTGTGGGACCGCTGGGCCCCCAGCGATGGCGACCCTGTGGGGAGGCCTTCT 160
Qy        130 TCGGCTTGGCTCCTTGCTCAGCCTGTCGTGCCTGGCGCTTTCCGTGCTGCTGCTGGCGCA 189
Db        161 TCGGCTTGGCTCCTTGCTCAGCCTGTCGTGCCTGGCGCTTTCCGTGCTGCTGCTGGCGCA 220
Qy        190 GCTGTCAGACGCCGCCAAGAATTTCGAGGATGTCAGATGTAAATGTATCTGCCCTCCCTA 249
Db        221 GCTGTCAGACGCCGCCAAGAATTTCGAGGATGTCAGATGTAAATGTATCTGCCCTCCCTA 280
Qy        250 TAAAGAAAATTCTGGGCATATTTATAATAAGAACATATCTCAGAAAGATTGTGATTGCCT 309
Db        281 TAAAGAAAATTCTGGGCATATTTATAATAAGAACATATCTCAGAAAGATTGTGATTGCCT 340
Qy        310 TCATGTTGTGGAGCCCATGCCTGTGCGGGGGCCTGATGTAGAAGCATACTGTCTACGCTG 369
Db        341 TCATGTTGTGGAGCCCATGCCTGTGCGGGGGCCTGATGTAGAAGCATACTGTCTACGCTG 400
Qy        370 TGAATGCAAATATGAAGAAAGAAGCTCTGTCACAATCAAGGTTACCATTATAATTTATCT 429
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Db        401 TGAATGCAAATATGAAGAAAGAAGCTCTGTCACAATCAAGGTTACCATTATAATTTATCT 460

Qy        430 CTCCATTTTGGGCCTTCTACTTCTGTACATGGTATATCTTACTCTGGTTGAGCCCATACT 489
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        461 CTCCATTTTGGGCCTTCTACTTCTGTACATGGTATATCTTACTCTGGTTGAGCCCATACT 520

Qy        490 GAAGAGGCGCCTCTTTGGACATGCACAGTTGATACAGAGTGATGATGATATTGGGGATCA 549
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        521 GAAGAGGCGCCTCTTTGGACATGCACAGTTGATACAGAGTGATGATGATATTGGGGATCA 580

Qy        550 CCAGCCTTTTGCAAATGCACACGATGTGCTAGCCCGCTCCCGCAGTCGAGCCAACGTGCT 609
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Db        581 CCAGCCTTTTGCAAATGCACACGATGTGCTAGCCCGCTCCCGCAGTCGAGCCAACGTGCT 640

Qy        610 GAACAAGGTAGAATATGCACAGCAGCGCTGGAAGCTTCAAGTCCAAGAGCAGCGAAAGTC 669
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Db        641 GAACAAGGTAGAATATGCACAGCAGCGCTGGAAGCTTCAAGTCCAAGAGCAGCGAAAGTC 700

Qy        670 TGTCTTTGACCGGCATGTTGTCCTCAGCTAATTGGGAATTGAATTCAAGGTGACTAGAAA 729
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Db        701 TGTCTTTGACCGGCATGTTGTCCTCAGCTAATTGGGAATTGAATTCAAGGTGACTAGAAA 760

Qy        730 GAAACAGGCAGACAACTGGAAAGAACTGACTGGGTTTTGCTGGGTTTCATTTTAATACCT 789
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        761 GAAACAGGCAGACAACTGGAAAGAACTGACTGGGTTTTGCTGGGTTTCATTTTAATACCT 820

Qy        790 TGTTGATTTCACCAACTGTTGCTGGAAGATTCAAAACTGGAAGCAAAAACTTGCTTGATT 849
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Db        821 TGTTGATTTCACCAACTGTTGCTGGAAGATTCAAAACTGGAAGCAAAAACTTGCTTGATT 880

Qy        850 TTTTTTTCTTGTTAACGTAATAATAGAGACATTTTTAAAAGCACACAGCTCAAAGTCAGC 909
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Db        881 TTTTTTTCTTGTTAACGTAATAATAGAGACATTTTTAAAAGCACACAGCTCAAAGTCAGC 940

Qy        910 CAATAAGTCTTTTCCTATTTGTGACTTTTACTAATAAAAATAAATCTGCCTGTAAATTAT 969
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Db        941 CAATAAGTCTTTTCCTATTTGTGACTTTTACTAATAAAAATAAATCTGCCTGTAAATTAT 1000

Qy        970 CTTGAAGTCCTTTACCTGGAACAAGCACTCTCTTTTTCACCACATAGTTTTAACTTGACT 1029
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1001 CTTGAAGTCCTTTACCTGGAACAAGCACTCTCTTTTTCACCACATAGTTTTAACTTGACT 1060

Qy       1030 TTCAAGATAATTTTCAGGGTTTTTGTTGTTGTTGTTTTTTGTTTGTTTGTTTTGGTGGGA 1089
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1061 TTCAAGATAATTTTCAGGGTTTTTGTTGTTGTTGTTTTTTGTTTGTTTGTTTTGGTGGGA 1120

Qy       1090 GAGGGGAGGGATGCCTGGGAAGTGGTTAACAACTTTTTTCAAGTCACTTTACTAAACAAA 1149
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1121 GAGGGGAGGGATGCCTGGGAAGTGGTTAACAACTTTTTTCAAGTCACTTTACTAAACAAA 1180

Qy       1150 CTTTTGTAAATAGACCTTACCTTCTATTTTCGAGTTTCATTTATATTTTGCAGTGTAGCC 1209
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1181 CTTTTGTAAATAGACCTTACCTTCTATTTTCGAGTTTCATTTATATTTTGCAGTGTAGCC 1240

Qy       1210 AGCCTCATCAAAGAGCTGACTTACTCATTTGACTTTTGCACTGACTGTATTATCTGGGTA 1269
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1241 AGCCTCATCAAAGAGCTGACTTACTCATTTGACTTTTGCACTGACTGTGTTATCTGGGTA 1300

Qy       1270 TCTGCTGTGTCTGCACTTCATGGTAAACGGGATCTAAAATGCCTGGTGGCTTTTCACAAA 1329
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1301 TCTGCTGTGTCTGCACTTCATGGTAAACGGGATCTAAAATGCCTGGTGGCTTTTCACAAA 1360

Qy       1330 AAGCAGATTTTCTTCATGTACTGTGATGTCTGATGCAATGCATCCTAGAACAAACTGGCC 1389
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1361 AAGCAGATTTTCTTCATGTACTGTGATGTCTGATGCAATGCATCCTAGAACAAACTGGCC 1420

Qy       1390 ATTTGCTAGTTTACTCTAAAGACTAAACATAGTCTTGGTGTGTGTGGTCTTACTCATCTT 1449
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1421 ATTTGCTAGTTTACTCTAAAGACTAAACATAGTCTTGGTGTGTGTGGTCTTACTCATCTT 1480

Qy       1450 CTAGTACCTTTAAGGACAAATCCTAAGGACTTGGACACTTGCAATAAAGAAATTTTATTT 1509
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||

Db       1481 CTAGTACCTTTAAGGACAAATCCTAAGGACTTGGACACTTGCAATAAAGAAATTTTATTT 1540

Qy       1510 TAAACCCAAGCCTCCCTGGATTGATAATATATACACATTTGTCAGCATTTCCGGTCGTGG 1569
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1541 TAAACCCAAGCCTCCCTGGATTGATAATATATACACATTTGTCAGCATTTCCGGTCGTGG 1600

Qy       1570 TGAGAGGCAGCTGTTTGAGCTCCAATATGTGCAGCTTTGAACTAGGGCTGGGGTTGTGGG 1629
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1601 TGAGAGGCAGCTGTTTGAGCTCCAATGTGTGCAGCTTTGAACTAGGGCTGGGGTTGTGGG 1660

Qy       1630 TGCCTCTTCTGAAAGGTCTAACCATTATTGGATAACTGGCTTTTTTCTTCCTATGTCCTC 1689
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1661 TGCCTCTTCTGAAAGGTCTAACCATTATTGGATAACTGGCTTTTTTCT-------TCCTC 1713

Qy       1690 TTTGGAATGTAACAATAAAAATAATTTTTGAAACATCAA 1728
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Db       1714 TTTGGAATGTAACAATAAAAATAATTTTTGAAACATCCA 1752
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RESULT 9
BD127721

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LOCUS       BD127721                1694 bp    DNA     linear   PAT 18-SEP-2002
DEFINITION  Primer for synthesizing full-length cDNA and use thereof.
ACCESSION   BD127721
VERSION     BD127721.1  GI:23222666
KEYWORDS    JP 2002017375-A/3152.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 1694)
  AUTHORS   Ota,T., Nishikawa,T., Isogai,T., Hayashi,K., Ishii,S., Kawai,Y.,
            Wakamatsu,A., Sugiyama,T., Nagai,K., Kojima,S., Otsuki,T. and
            Koga,H.
  TITLE     Primer for synthesizing full-length cDNA and use thereof
  JOURNAL   Patent: JP 2002017375-A 3152 22-JAN-2002;
            HELIX RESEARCH INSTITUTE
COMMENT     OS   Homo sapiens (human)
            PN   JP 2002017375-A/3152
            PD   22-JAN-2002
            PF   07-JUL-2000 JP 2000253172
            PI   TOSHIO OTA,TETSUO NISHIKAWA,TAKAO ISOGAI,KOJI HAYASHI,SHIZUKO
            PI   ISHII,
            PI   YURI KAWAI,AI WAKAMATSU,TOMOYASU SUGIYAMA,KEIICHI NAGAI, PI
            SHINICHI KOJIMA,
            PI   TETSUJI OTSUKI,HISASHI KOGA
            PC
            C12N15/09,C07K14/47,C07K16/18,C12N1/15,C12N1/19,C12N1/21,C12N5/ PC
             10,
            PC   C12P21/02,C12Q1/68//C12P21/08,G06F17/30,C12N15/00,C12N5/00 CC
             Primer for synthesizing full-length cDNA and use thereof FH   Key
                     Location/Qualifiers
            FT   CDS             (79). .(672).
FEATURES             Location/Qualifiers
     source          1. .1694
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ORIGIN
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  Query Match           96.8%;  Score 1672.2;  DB 6;  Length 1694;
  Best Local Similarity   99.4%;  Pred. No. 0;
  Matches 1691;  Conservative    0;  Mismatches    3;  Indels    7;  Gaps    1;

Qy         26 AGCCTGAGCCTGAGCCTGAGCCCGAGCCGGGAGCCGGTCGCGGGGGCTCCGGGCTGTGGG 85
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 AGCCTGAGCCTGAGCCTGAGCCCGAGCCGGGAGCCGGTCGCGGGGGCTCCGGGCTGTGGG 60

Qy         86 ACCGCTGGGCCCCCAGCGATGGCGACCCTGTGGGGAGGCCTTCTTCGGCTTGGCTCCTTG 145
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 ACCGCTGGGCCCCCAGCGATGGCGACCCTGTGGGGAGGCCTTCTTCGGCTTGGCTCCTTG 120

Qy        146 CTCAGCCTGTCGTGCCTGGCGCTTTCCGTGCTGCTGCTGGCGCAGCTGTCAGACGCCGCC 205
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Db      121 CTCAGCCTGTCGTGCCTGGCGCTTTCCGTGCTGCTGCTGGCGCAGCTGTCAGACGCCGCC 180
Qy      206 AAGAATTTCGAGGATGTCAGATGTAAATGTATCTGCCCTCCCTATAAAGAAAATTCTGGG 265
Db      181 AAGAATTTCGAGGATGTCAGATGTAAATGTATCTGCCCTCCCTATAAAGAAAATTCTGGG 240
Qy      266 CATATTTATAATAAGAACATATCTCAGAAAGATTGTGATTGCCTTCATGTTGTGGAGCCC 325
Db      241 CATATTTATAATAAGAACATATCTCAGAAAGATTGTGATTGCCTTCATGTTGTGGAGCCC 300
Qy      326 ATGCCTGTGCGGGGGCCTGATGTAGAAGCATACTGTCTACGCTGTGAATGCAAATATGAA 385
Db      301 ATGCCTGTGCGGGGGCCTGATGTAGAAGCATACTGTCTACGCTGTGAATGCAAATATGAA 360
Qy      386 GAAAGAAGCTCTGTCACAATCAAGGTTACCATTATAATTTATCTCTCCATTTTGGGCCTT 445
Db      361 GAAAGAAGCTCTGTCACAATCAAGGTTACCATTATAATTTATCTCTCCATTTTGGGCCTT 420
Qy      446 CTACTTCTGTACATGGTATATCTTACTCTGGTTGAGCCCATACTGAAGAGGCGCCTCTTT 505
Db      421 CTACTTCTGTACATGGTATATCTTACTCTGGTTGAGCCCATACTGAAGAGGCGCCTCTTT 480
Qy      506 GGACATGCACAGTTGATACAGAGTGATGATGATGATATTGGGGATCACCAGCCTTTTGCAAAT 565
Db      481 GGACATGCACAGTTGATACAGAGTGATGATGATGATATTGGGGATCACCAGCCTTTTGCAAAT 540
Qy      566 GCACACGATGTGCTAGCCCGCTCCCGCAGTCGAGCCAACGTGCTGAACAAGGTAGAATAT 625
Db      541 GCACACGATGTGCTAGCCCGCTCCCGCAGTCGAGCCAACGTGCTGAACAAGGTAGAATAT 600
Qy      626 GCACAGCAGCGCTGGAAGCTTCAAGTCCAAGAGCAGCGAAAGTCTGTCTTTGACCGGCAT 685
Db      601 GCACAGCAGCGCTGGAAGCTTCAAGTCCAAGAGCAGCGAAAGTCTGTCTTTGACCGGCAT 660
Qy      686 GTTGTCCTCAGCTAATTGGGAATTGAATTCAAGGTGACTAGAAAGAAACAGGCAGACAAC 745
Db      661 GTTGTCCTCAGCTAATTGGGAATTGAATTCAAGGTGACTAGAAAGAAACAGGCAGACAAC 720
Qy      746 TGGAAAGAACTGACTGGGTTTTGCTGGGTTTCATTTTAATACCTTGTTGATTTCACCAAC 805
Db      721 TGGAAAGAACTGACTGGGTTTTGCTGGGTTTCATTTTAATACCTTGTTGATTTCACCAAC 780
Qy      806 TGTTGCTGGAAGATTCAAAACTGGAAGCAAAAACTTGCTTGATTTTTTTTTCTTGTTAAC 865
Db      781 TGTTGCTGGAAGATTCAAAACTGGAAGCAAAAACTTGCTTGATTTTTTTTTCTTGTTAAC 840
Qy      866 GTAATAATAGAGACATTTTTAAAAGCACACAGCTCAAAGTCAGCCAATAAGTCTTTTCCT 925
Db      841 GTAATAATAGAGACATTTTTAAAAGCACACAGCTCAAAGTCAGCCAATAAGTCTTTTCCT 900
Qy      926 ATTTGTGACTTTTACTAATAAAAATAAATCTGCCTGTAAATTATCTTGAAGTCCTTTACC 985
Db      901 ATTTGTGACTTTTACTAATAAAAATAAATCTGCCTGTAAATTATCTTGAAGTCCTTTACC 960
Qy      986 TGGAACAAGCACTCTCTTTTTCACCACATAGTTTTAACTTGACTTTCAAGATAATTTTCA 1045
Db      961 TGGAACAAGCACTCTCTTTTTCACCACATAGTTTTAACTTGACTTTCAAGATAATTTTCA 1020
Qy     1046 GGGTTTTTGTTGTTGTTGTTTTTTGTTTGTTTGTTTTGGTGGGAGAGGGGAGGGATGCCT 1105
Db     1021 GGGTTTTTGTTGTTGTTGTTTTTTGTTTGTTTGTTTTGGTGGGAGAGGGGAGGGATGCCT 1080
Qy     1106 GGGAAGTGGTTAACAACTTTTTTCAAGTCACTTTACTAAACAAACTTTTGTAAATAGACC 1165
Db     1081 GGGAAGTGGTTAACAACTTTTTTCAAGTCACTTTACTAAACAAACTTTTGTAAATAGACC 1140
Qy     1166 TTACCTTCTATTTTCGAGTTTCATTTATATTTTGCAGTGTAGCCAGCCTCATCAAAGAGC 1225
Db     1141 TTACCTTCTATTTTCGAGTTTCATTTATATTTTGCAGTGTAGCCAGCCTCATCAAAGAGC 1200
Qy     1226 TGACTTACTCATTTGACTTTTGCACTGACTGTATTATCTGGGTATCTGCTGTGTCTGCAC 1285
Db     1201 TGACTTACTCATTTGACTTTTGCACTGACTGTATTATCTGGGTATCTGCTGTGTCTGCAC 1260
Qy     1286 TTCATGGTAAACGGGATCTAAAATGCCTGGTGGCTTTTCACAAAAAGCAGATTTTCTTCA 1345
Db     1261 TTCATGGTAAACGGGATCTAAAATGCCTGGTGGCTTTTCACAAAAAGCAGATTTTCTTCA 1320
Qy     1346 TGTACTGTGATGTCTGATGCAATGCATCCTAGAACAAACTGGCCATTTGCTAGTTTACTC 1405
Db     1321 TGTACTGTGATGTCTGATGCAATGCATCCTAGAACAAACTGGCCATTTGCTAGTTTACTC 1380
Qy     1406 TAAAGACTAAACATAGTCTTGGTGTGTGTGGTCTTACTCATCTTCTAGTACCTTTAAGGA 1465
Db     1381 TAAAGACTAAACATAGTCTTGGTGTGTGTGGTCTTACTCATCTTCTAGTACCTTTAAGGA 1440
Qy     1466 CAAATCCTAAGGACTTGGACACTTGCAATAAAGAAATTTTATTTTAAACCCAAGCCTCCC 1525
Db     1441 CAAATCCTAAGGACTTGGACACTTGCAATAAAGAAATTTTATTTTAAACCCAAGCCTCCC 1500
Qy     1526 TGGATTGATAATATATACACATTTGTCAGCATTTCCGGTCGTGGTGAGAGGCAGCTGTTT 1585
Db     1501 TGGATTGATAATATATACACATTTGTCAGCATTTCCGGTCGTGGTGAGAGGCAGCTGTTT 1560
Qy     1586 GAGCTCCAATATGTGCAGCTTTGAACTAGGGCTGGGGTTGTGGGTGCCTCTTCTGAAAGG 1645
Db     1561 GAGCTCCAATGTGTGCAGCTTTGAACTAGGGCTGGGGTTGTGGGTGCCTCTTCTGAAAGG 1620
Qy     1646 TCTAACCATTATTGGATAACTGGCTTTTTTCTTCCTATGTCCTCTTTGGAATGTAACAAT 1705
Db     1621 TCTAACCATTATTGGATAACTGGCTTTTTTCT-------TCCCCTTTGGAATGTAACAAT 1673
Qy     1706 AAAAATAATTTTTGAAACATC 1726
Db     1674 AAAAATAATTTTCGAAACATC 1694
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RESULT 10
AK074677

LOCUS	AK074677 1694 bp mRNA linear PRI 03-SEP-2002
DEFINITION	Homo sapiens cDNA FLJ90196 fis, clone MAMMA1001344.
ACCESSION	AK074677
VERSION	AK074677.1 GI:22760273
KEYWORDS	oligo capping; fis (full insert sequence).
SOURCE	Homo sapiens (human)
ORGANISM	Homo sapiens Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE	1
AUTHORS	Isogai,T., Ota,T., Nishikawa,T., Hayashi,K., Otsuki,T., Sugiyama,T., Suzuki,Y., Nagai,K., Sugano,S., Ishii,S., Kawai-Hio,Y., Saito,K., Yamamoto,J., Wakamatsu,A., Nakamura,Y., Kojima,S., Nagahari,K., Masuho,Y., Ono,T., Okano,K., Yoshikawa,Y., Aotsuka,S., Sasaki,N., Hattori,A., Okumura,K., Iwayanagi,T. and Ninomiya,K.
TITLE	NEDO human cDNA sequencing project
JOURNAL	Unpublished
REFERENCE	2 (bases 1 to 1694)
AUTHORS	Isogai,T. and Otsuki,T.
TITLE	Direct Submission
JOURNAL	Submitted (25-MAR-2002) Takao Isogai, Helix Research Institute, Genomics Laboratory; 1532-3 Yana, Kisarazu, Chiba 292-0812, Japan (E-mail:genomics@hri.co.jp, Tel:81-438-52-3975, Fax:81-438-52-3986)
COMMENT	NEDO human cDNA sequencing project supported by Ministry of Economy, Trade and Industry of Japan; cDNA full insert sequencing: Research Association for Biotechnology; cDNA library construction: Institute of Medical Science, University of Tokyo, Laboratory of Genome Structure, Human Genome Center; cDNA 5'- & 3'-end one pass sequencing and clone selection: Helix Research Institute (supported by Japan Key Technology Center etc.).
FEATURES	Location/Qualifiers
source	1. .1694 /organism="Homo sapiens" /mol_type="mRNA" /db_xref="taxon:9606"

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ORIGIN

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  Matches 1691;  Conservative    0;  Mismatches    3;  Indels    7;  Gaps    1;

Qy         26 AGCCTGAGCCTGAGCCTGAGCCCGAGCCGGGAGCCGGTCGCGGGGGGCTCCGGGCTGTGGG 85
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Db          1 AGCCTGAGCCTGAGCCTGAGCCCGAGCCGGGAGCCGGTCGCGGGGGCTCCGGGCTGTGGG 60

Qy         86 ACCGCTGGGCCCCCAGCGATGGCGACCCTGTGGGGAGGCCTTCTTCGGCTTGGCTCCTTG 145
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Qy        206 AAGAATTTCGAGGATGTCAGATGTAAATGTATCTGCCCTCCCTATAAAGAAAATTCTGGG 265
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Qy        326 ATGCCTGTGCGGGGGCCTGATGTAGAAGCATACTGTCTACGCTGTGAATGCAAATATGAA 385
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Qy        386 GAAAGAAGCTCTGTCACAATCAAGGTTACCATTATAATTTATCTCTCCATTTTGGGCCTT 445
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Qy        446 CTACTTCTGTACATGGTATATCTTACTCTGGTTGAGCCCATACTGAAGAGGCGCCTCTTT 505
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Qy        806 TGTTGCTGGAAGATTCAAAACTGGAAGCAAAAACTTGCTTGATTTTTTTTTCTTGTTAAC 865
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Qy        926 ATTTGTGACTTTTACTAATAAAAATAAATCTGCCTGTAAATTATCTTGAAGTCCTTTACC 985
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RESULT 11
AR352701
LOCUS       AR352701                1734 bp    DNA     linear   PAT 17-AUG-2003
DEFINITION  Sequence 108 from patent US 6590075.
ACCESSION   AR352701
VERSION     AR352701.1  GI:33757959
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
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REFERENCE   1  (bases 1 to 1734)
  AUTHORS   Ruben,S.M., Rosen,C.A., Fischer,C.L., Soppet,D.R., Carter,K.C.,
            Bednarik,D.P., Endress,G.A., Yu,G.-L., Ni,J., Feng,P., Young,P.E.,
            Greene,J.M., Ferrie,A.M., Duan,R., Hu,J.-S., Florence,K.A.,
            Olsen,H.S., Ebner,R., Brewer,L.A. and Shi,Y.
  TITLE     Secreted protein HODAZ50
  JOURNAL   Patent: US 6590075-A 108 08-JUL-2003;
FEATURES             Location/Qualifiers
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ORIGIN

  Query Match             95.4%;  Score 1649.2;  DB 6;  Length 1734;
  Best Local Similarity   99.1%;  Pred. No. 0;
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Qy        185 GCGCAGCTGTCAGACGCCGCCAAGAATTTCGAGGATGTCAGATGTAAATGTATCTGCCCT 244
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Qy        245 CCCTATAAAGAAAATTCTGGGCATATTTATAATAAGAACATATCTCAGAAAGATTGTGAT 304
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Db        780 TAATACCTTGTTGATTTCACCAACTGTTGCTGGAAGATTCAAAACTGGAAGCAAAAACTT 839

Qy        842 GCTTGATTTTTTTTTCTTGTTAACGTAATAATAGAGACATTTTTAAAAGCACACAGCTCA 901
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Qy        902 AAGTCAGCCAATAAGTCTTTTCCTATTTGTGACTTTTACTAATAAAAATAAATCTGCCTG 961
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Db        900 AAGTCAGCCAATAAGTCTTTTCCTATTTGTGACTTTTACTAATAAAAATAAATCTGCCTG 959

Qy        962 TAAATTATCTTGAAGTCCTTTACCTGGAACAAGCACTCTCTTTTTCACCACATAGTTTTA 1021
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Qy       1022 ACTTGACTTTCAAGATAATTTTCAGGGTTTTTGTTGTTGTTGTTTTTTGTTTGTTTGTTT 1081
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Qy       1442 CTCATCTTCTAGTACCTTTAAGGACAAATCCTAAGGACTTGGACACTTGCAATAAAGAAA 1501
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RESULT 12
BD195646
LOCUS       BD195646               1734 bp    DNA     linear   PAT 17-JUL-2003
DEFINITION  70 human secreted proteins.
ACCESSION   BD195646
VERSION     BD195646.1  GI:33005416
KEYWORDS    JP 2002519990-A/107.
SOURCE      unidentified
  ORGANISM  unidentified
            unclassified.
REFERENCE   1  (bases 1 to 1734)
  AUTHORS   Ruben,S.M., Rosen,C.A., Fischer,C.L., Soppet,D.R., Carter,K.C.,
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          Bednarik,D.P., Endress,G.A., Yu,G.L., N,J., Feng,P., Young,P.E.,
          Greene,J.M., Ferrie,A.M., Duan,R., Hu,J.S., Florence,K.A.,
          Olsen,H.S., Ebner,R., Brewer,L.A., Moore,P.A., Shi,Y.,
          Lafleur,D.W., Li,Y., Zeng,Z. and Kyaw,H.
  TITLE   70 human secreted proteins
  JOURNAL Patent: JP 2002519990-A 107 02-JUL-2002;
          HUMAN GENOME SCIENCES INC
COMMENT   OS   Unidentified
          PN   JP 2002519990-A/107
          PD   02-JUL-2002
          PF   06-MAR-1998 JP 1998538875
          PR   07-MAR-1997 US    60/040162,07-MAR-1997 US    60/040333 PR
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          PI   PING FENG,PAUL E YOUNG,JOHN M GREENE,ANN
          M FERRIE,ROXANNE DUAN,
          PI   JING SHAN HU,KIMBERLY A FLORENCE,HENRIK
          S OLSEN,REINHARD EBNER,
          PI   LAURIE A BREWER,PAUL A MOORE,YANGGU SHI,DAVID W LAFLEUR PI
          ,YI LI,ZHIZHEN ZENG,
          PI   HLA KYAW
          PC   C12N15/12,C12N5/10,C12N1/21,C07K14/47,C07K16/18,C12Q1/68, PC
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VERSION     AR352639.1  GI:33757897
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 1772)
  AUTHORS   Ruben,S.M., Rosen,C.A., Fischer,C.L., Soppet,D.R., Carter,K.C.,
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RESULT 14
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LOCUS BD195584 1772 bp DNA linear PAT 17-JUL-2003
DEFINITION 70 human secreted proteins.
ACCESSION BD195584
VERSION BD195584.1 GI:33005354
KEYWORDS JP 2002519990-A/45.
SOURCE unidentified
ORGANISM unidentified
unclassified.
REFERENCE 1 (bases 1 to 1772)
AUTHORS Ruben,S.M., Rosen,C.A., Fischer,C.L., Soppet,D.R., Carter,K.C., Bednarik,D.P., Endress,G.A., Yu,G.L., N,J., Feng,P., Young,P.E., Greene,J.M., Ferrie,A.M., Duan,R., Hu,J.S., Florence,K.A., Olsen,H.S., Ebner,R., Brewer,L.A., Moore,P.A., Shi,Y.,
Lafleur,D.W., Li,Y., Zeng,Z. and Kyaw,H.
TITLE 70 human secreted proteins
JOURNAL Patent: JP 2002519990-A 45 02-JUL-2002;
HUMAN GENOME SCIENCES INC
COMMENT OS Unidentified
PN JP 2002519990-A/45
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PI PING FENG,PAUL E YOUNG,JOHN M GREENE,ANN
M FERRIE,ROXANNE DUAN,
PI JING SHAN HU,KIMBERLY A FLORENCE,HENRIK
S OLSEN,REINHARD EBNER,
PI LAURIE A BREWER,PAUL A MOORE,YANGGU SHI,DAVID W LAFLEUR PI
,YI LI,ZHIZHEN ZENG,
PI HLA KYAW
PC C12N15/12,C12N5/10,C12N1/21,C07K14/47,C07K16/18,C12Q1/68, PC
G01N33/50,
PC G01N33/53,G01N33/68,A61K38/17
CC Strandedness: Double;
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CC 70 human secreted proteins
FH Key Location/Qualifiers

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RESULT 15
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VERSION     BD218614.1  GI:33028384
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            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 1772)
  AUTHORS   Ruben,S.M., Komatsoulis,G., Duan,R.D., Rosen,C.A., Moore,P.A.,
            Shi,Y., Lafleur,D.W., Ebner,R., Olsen,H.S., Brewer,L.A.,
            Florence,K.A., Young,P.E., Mucenski,M., Endress,G.A. and
            Soppet,D.R.
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            PI   STEVEN M RUBEN,GEORGE KOMATSOULIS,ROXANNE
            D DUAN,CRAIG A ROSEN,
            PI   PAUL A MOORE,YANGGU SHI,DAVID W LAFLEUR,REINHARD EBNER,HENRIK
            PI   S OLSEN,
            PI   LAURIE A BREWER,KIMBERLY A FLORENCE,PAUL E YOUNG,MICHAEL  PI
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ORIGIN

  Query Match             92.0%;  Score 1589.6;  DB 6;  Length 1772;
  Best Local Similarity   98.6%;  Pred. No. 0;
  Matches 1711;  Conservative    0;  Mismatches    9;  Indels   16;  Gaps   10;

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GenCore version 5.1.6

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Gapop 10.0 , Gapext 1.0

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Minimum DB seq length: 0
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Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

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	4	931.2	53.9	1201	13	BX425270	BX425270 BX425270
c	5	913.8	52.9	1201	9	AL562476	AL562476 AL562476
	6	904	52.3	1201	13	BX440898	BX440898 BX440898
c	7	903.4	52.3	1201	9	AL550557	AL550557 AL550557
	8	899.8	52.1	1642	11	AK077253	AK077253 Mus muscu
	9	893.8	51.7	1063	12	BM924942	BM924942 AGENCOURT
c	10	893.4	51.7	962	9	AL567498	AL567498 AL567498
	11	891.4	51.6	1201	13	BX439642	BX439642 BX439642
	12	890.8	51.6	1201	9	AL552487	AL552487 AL552487
	13	888.6	51.4	1190	9	AL552032	AL552032 AL552032
c	14	884	51.2	1201	9	AL576084	AL576084 AL576084
	15	869.2	50.3	953	9	AL540345	AL540345 AL540345
	16	868.4	50.3	1105	12	BM924900	BM924900 AGENCOURT
	17	865.4	50.1	1201	9	AL550588	AL550588 AL550588
	18	854.2	49.4	961	9	AL538778	AL538778 AL538778
	19	851.4	49.3	1020	9	AL543744	AL543744 AL543744
	20	851.4	49.3	1201	13	BX364690	BX364690 BX364690
c	21	848.8	49.1	854	9	AL546065	AL546065 AL546065
	22	839.8	48.6	929	13	BX438705	BX438705 BX438705
	23	838.8	48.5	1029	12	BM556889	BM556889 AGENCOURT
c	24	826.6	47.8	916	13	BX371884	BX371884 BX371884
	25	826.4	47.8	1772	11	AK049882	AK049882 Mus muscu
	26	814.4	47.1	900	13	BU145696	BU145696 AGENCOURT
	27	809	46.8	827	12	BI907871	BI907871 603066863
c	28	806.8	46.7	1194	9	AL575778	AL575778 AL575778
	29	804.6	46.6	962	12	BM921821	BM921821 AGENCOURT
	30	802.2	46.4	950	13	BU552570	BU552570 AGENCOURT
	31	800	46.3	928	13	BX403296	BX403296 BX403296
	32	799.2	46.2	1201	13	BX420531	BX420531 BX420531
	33	797.8	46.2	904	12	BI833099	BI833099 603090811
c	34	789.6	45.7	1201	13	BX397421	BX397421 BX397421
c	35	787.2	45.6	1201	13	BX364689	BX364689 BX364689
	36	777.6	45.0	1407	11	AK009147	AK009147 Mus muscu
c	37	765.6	44.3	1201	13	BX425269	BX425269 BX425269
	38	762.6	44.1	911	14	CA454836	CA454836 AGENCOURT
c	39	758.4	43.9	1002	9	AL543902	AL543902 AL543902
	40	751.4	43.5	785	12	BI598275	BI598275 603245455
	41	748.6	43.3	924	13	BX464778	BX464778 BX464778
	42	747	43.2	747	12	BI756642	BI756642 603024028
	43	731.2	42.3	938	14	CD109149	CD109149 AGENCOURT
	44	724.6	41.9	1121	12	BM918858	BM918858 AGENCOURT
	45	722.8	41.8	879	13	BQ224552	BQ224552 AGENCOURT

ALIGNMENTS

RESULT 1
AL542404
LOCUS AL542404 1045 bp mRNA linear EST 12-MAY-2003
DEFINITION AL542404 Homo sapiens PLACENTA Homo sapiens cDNA clone CS0DE010YN08 5-PRIME, mRNA sequence.
ACCESSION AL542404
VERSION AL542404.2 GI:30547515
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 1045)
AUTHORS Li,W.B., Gruber,C., Jessee,J. and Polayes,D.
TITLE Full-length cDNA libraries and normalization
JOURNAL Unpublished (2001)
COMMENT On Feb 15, 2001 this sequence version replaced gi:12874416.
Contact: Genoscope
Genoscope - Centre National de Sequencage
BP 191 91006 EVRY cedex - France
Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr
Library was constructed by Life Technologies, a division of Invitrogen. This sequence belongs to sequence cluster 6242.f For more information about this cluster, see
http://www.genoscope.cns.fr/
cgi-bin/cluster.cgi?seq=CS0DE010DG04QP1&cluster=6242.f. Contact :
Feng Liang Email : fliang@lifetech.com URL :

```
           http://fulllength.invitrogen.com/ InVitroGen Corporation 1600
           Faraday Avenue Genoscope sequence ID : CS0DE010DG04QP1.
FEATURES             Location/Qualifiers
     source          1. .1045
                     /organism="Homo sapiens"
                     /mol_type="mRNA"
                     /db_xref="taxon:9606"
                     /clone="CS0DE010YN08"
                     /tissue_type="PLACENTA"
                     /clone_lib="Homo sapiens PLACENTA"
                     /note="Vector: pCMVSPORT_6; 1st strand cDNA was primed
                     with a NotI-oligo(dT) primer. Five prime end enriched,
                     double-strand cDNA was digested with Not I and cloned into
                     the Not I and EcoRV sites of the pCMVSPORT 6 vector.
                     Library was not normalized."
ORIGIN

  Query Match             54.8%;  Score 947.4;  DB 9;  Length 1045;
  Best Local Similarity   95.2%;  Pred. No. 1.6e-169;
  Matches  949;  Conservative   40;  Mismatches    6;  Indels    2;  Gaps    2;

Qy         20 TGCCTGAGCCTGAGCCTGAGCCTGAGCCCGAGCCGGGAGCCGGTCGCGGGGGCTCCGGGC 79
              | || |   |||||::|||||:|||||:|||||:|||||::|||||||||||:|||||||
Db         50 TCCCGGGATCTGAGSSTGAGCSTGAGCSCGAGCSGGGAGSSGGTCGCGGGGGSTCCGGGC 109

Qy         80 TGTGGGACCGCTGGGCCCCCAGCGATGGCGACCCTGTGGGGAGGCCTTCTTCGGCTTGGC 139
              |||||||||||||||||:|||||||||||:|||||||||||||||||:||||||||:|||||
Db        110 TGTGGGACCGCTGGGCSCCCAGCGATGGSGACCCTGTGGGGAGGCSTTCTTCGGSTTGGC 169

Qy        140 TCCTTGCTCAGCCTGTCGTGCCTGGCGCTTTCCGTGCTGCTGCTGGCGCAGCTGTCAGAC 199
              |||||||||||||||||||||||||||||:||||||||||:||:||::||:|||| |||:|||:
Db        170 TCCTTGCTCAGCCTGTCGTGCCTGGSGCTTTCCGTGSTGSTGSKGGSGCAG-TGTSAGAS 228

Qy        200 GCCGCCAAGAATTTCGAGGATGTCAGATGTAAATGTATCTGCCCTCCCTATAAAGAAAAT 259
              |:|||||||||||:||||||||:|||||||||||||||||||||:|||||||||||||||
Db        229 GSCGCCAAGAATTTSGAGGATGTSAGATGTAAATGTATCTGCCCTCSCTATAAAGAAAAT 288

Qy        260 TCTGGGCATATTTATAATAAGAACATATCTCAGAAAGATTGTGATTGCCTTCATGTTGTG 319
              |||||||||||||||||||||||||||||:|||||||||||||||:|||||||||||||
Db        289 TCTGGGCATATTTATAATAAGAACATATCTSAGAAAGATTGTGATTGCSTTCATGTTGTG 348

Qy        320 GAGCCCATGCCTGTGCGGGGGCCTGATGTAGAAGCATACTGTCTACGCTGTGAATGCAAA 379
              ||||:|||||||||||||||||||||||||||||||||||||||||:||||||||||||
Db        349 GAGCSCATGCCTGTGCGGGGGCCTGATGTAGAAGCATACTGTCTACGSTGTGAATGCAAA 408

Qy        380 TATGAAGAAAGAAGCTCTGTCACAATCAAGGTTACCATTATAATTTATCTCTCCATTTTG 439
              |||||||||||||||||||:|||||||||||||||||||||||||||||||:|||||||
Db        409 TATGAAGAAAGAAGCTCTGTSACAATCAAGGTTACCATTATAATTTATCTCTSCATTTTG 468

Qy        440 GGCCTTCTACTTCTGTACATGGTATATCTTACTCTGGTTGAGCCCATACTGAAGAGGCGC 499
              |||||||||||||||||||||:|||||||||||||||||||||||||||||||||||||
Db        469 GGCCTTCTACTTCTGTACATGGTATATSTTACTCTGGTTGAGCCCATACTGAAGAGGCGC 528

Qy        500 CTCTTTGGACATGCACAGTTGATACAGAGTGATGATGATATTGGGGATCACCAGCCTTTT 559
              |||||||||||||||||||||||||||||||||||||||||||||:||||||:||||
Db        529 CTCTTTGGACATGCACAGTTGATACAGAGTGATGATGATATTGGGGATSACCAGCSTTTT 588

Qy        560 GCAAATGCACACGATGTGCTAGCCCGCTCCCGCAGTCGAGCCAACGTGCTGAACAAGGTA 619
              |:|||||||||||||||||||||||||||||:|||||||||||||||||||||||||||
Db        589 GSAAATGCACACGATGTGCTAGCCCGCTCCCGCAGTSGAGCCAACGTGCTGAACAAGGTA 648

Qy        620 GAATATGCACAGCAGCGCTGGAAGC-TTCAAGTCCAAGAGCAGCGAAAGTCTGTCTTTGA 678
              |||||||||||||||||:|||||| ||||||||||||||||||||||||||||||||||
Db        649 GAATATGCACAGCAGCGSTGGAAGCGTTCAAGTCCAAGAGCAGCGAAAGTCTGTCTTTGA 708

Qy        679 CCGGCATGTTGTCCTCAGCTAATTGGGAATTGAATTCAAGGTGACTAGAAAGAAACAGGC 738
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        709 CCGGCATGTTGTCCTCAGCTAATTGGGAATTGAATTCAAGGTGACTAGAAAGAAACAGGC 768

Qy        739 AGACAACTGGAAAGAACTGACTGGGTTTTGCTGGGTTTCATTTTAATACCTTGTTGATTT 798
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        769 AGACAACTGGAAAGAACTGACTGGGTTTTGCTGGGTTTCATTTTAATACCTTGTTGATTT 828

Qy        799 CACCAACTGTTGCTGGAAGATTCAAAACTGGAAGCAAAAACTTGCTTGATTTTTTTTTCT 858
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        829 CACCAACTGTTGCTGGAAGATTCAAAACTGGAAGCAAAAACTTGCTTGATTTTTTTTTCT 888

Qy        859 TGTTAACGTAATAATAGAGACATTTTTAAAAGCACACAGCTCAAAGTCAGCCAATAAGTC 918
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        889 TGTTAACGTAATAATAGAGACATTTTTAAAAGCACACAGCTCAAAGTCAGCCAATAAGTC 948

Qy        919 TTTTCCTATTTGTGACTTTTACTAATAAAAATAAATCTGCCTGTAAATTATCTTGAAGTC 978
              ||||||||||||||||||||||||||||||||||||:||:|||||||:||||||||||
Db        949 TTTTCCTATTTGTGACTTTTACTAATAAAAATAAATCKGCSTGTAAATKATCTTGAAGTC 1008

Qy        979 CTTTACCTGGAACAAGCACTCTCTTTTTCACCACATA 1015
              |||||||||| |||||||||||||||||||||||
Db       1009 CTTTACCTGGGAMAAGCACTCTCTTTTTCACCACATA 1045


RESULT 2
AL575462/c
LOCUS       AL575462               1180 bp    mRNA    linear   EST 01-JUN-2003
DEFINITION  AL575462 Homo sapiens PLACENTA COT 25-NORMALIZED Homo sapiens cDNA
            clone CS0DI060YL12 3-PRIME, mRNA sequence.
ACCESSION   AL575462
VERSION     AL575462.2  GI:31313770
KEYWORDS    EST.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 1180)
  AUTHORS   Li,W.B., Gruber,C., Jessee,J. and Polayes,D.
  TITLE     Full-length cDNA libraries and normalization
  JOURNAL   Unpublished (2001)
COMMENT     On Feb 16, 2001 this sequence version replaced gi:12936648.
            Contact: Genoscope
            Genoscope - Centre National de Sequencage
            BP 191 91006 EVRY cedex - France
            Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr
            Library was constructed by Life Technologies, a division of
            Invitrogen. This sequence belongs to sequence cluster 6242.f For
            more information about this cluster, see
            http://www.genoscope.cns.fr/
            cgi-bin/cluster.cgi?seq=CS0DI060DF06NP1&cluster=6242.f. Contact :
            Feng Liang Email : fliang@lifetech.com URL :
            http://fulllength.invitrogen.com/ InVitroGen Corporation 1600
            Faraday Avenue Genoscope sequence ID : CS0DI060DF06NP1.
FEATURES             Location/Qualifiers
     source          1. .1180
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                     /mol_type="mRNA"
                     /db_xref="taxon:9606"
                     /clone="CS0DI060YL12"
                     /tissue_type="PLACENTA COT 25-NORMALIZED"
                     /clone_lib="Homo sapiens PLACENTA COT 25-NORMALIZED"
                     /note="1st strand cDNA was primed with a NotI-oligo(dT)
                     primer. Five prime end enriched, double-strand cDNA was
                     digested with Not I and cloned into the Not I and EcoR V
                     sites of the pCMVSPORT 6 vector. Library was normalized."
ORIGIN

  Query Match             54.3%;  Score 938;  DB 9;  Length 1180;
  Best Local Similarity   94.6%;  Pred. No. 9.7e-168;
  Matches 1004;  Conservative   24;  Mismatches   26;  Indels    7;  Gaps    6;

Qy        630 AGCAGCGCTGGAAGCTTCAAGTCCAAGAGCAGCGAAAGTCTGTCTTTGACCGGCATGTTG 689
              | : : ||  | |:: |||||:||||||||:||||||||:|| ||::|||||||||||
Db       1058 ACMGSAGCSTGGARSCTCAAGYCCAAGAGCASCGAAAGTCTKTC-TTRMCCGGCATGTTG 1000

Qy        690 TCCTCAGCTAATTGGGAATTGAATTCAAGGTGACTAGAAAGAAACAGGCAGACAACTGGA 749
              |||||||||||||||:||||| ||| |:||:|||||||||||||||||||||||||||||
Db        999 CCCTCAGCTAATTGGGWATTGATTTC-ADGTKACTAGAAAGAAACAGGCAGACAACTGGA 941

Qy        750 AAGAACTGACTGGGTTTTGCTGGGTTTCATTTTAATACCTTGTTGATTT-CACCAACTGT 808
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Db        940 AAGAACTGACTGGGTTT--GCTGGKTTCATTTTAATACCTTGTTGATTTCCACCAACTGT 883

Qy        809 TGCTGGAAGATTCAAAACTGGAAGCAAAAACTTGCTTGATTTTTTTTTTCTTGTTAACGTA 868

Db        882 TGCTGGAAGATTCAAAACTGGAAGCAAAAACTTGCTTGA-TTTTTTTTCTTGTTAACGTA 824

Qy        869 ATAATAGAGACATTTTTAAAAGCACACAGCTCAAAGTCAGCCAATAAGTCTTTTCCTATT 928

Db        823 ATAATAGAGACATTTTTAAAAGCACACAGCTCAAAGTCAGCCAATAAGTCTTTTCCTATT 764

Qy        929 TGTGACTTTTACTAATAAAAATAAATCTGCCTGTAAATTATCTTGAAGTCCTTTACCTGG 988

Db        763 TGTGACTTTTACTAATAAAAATAAATCTGCCTGTAAATTATCTTGAAGTCCTTTACCTGG 704

Qy        989 AACAAGCACTCTCTTTTTCACCACATAGTTTTAACTTGACTTTCAAGATAATTTTCAGGG 1048

Db        703 AACAAGCACTCTCTTTTTCACCACATAGTTTTAACTTGACTTTCAAGATAATTYCCAGGG 644

Qy       1049 TTTTTGTTGTTGTTGTTTTTTGTTTGTTTGTTTTGGTGGGAGAGGGGAGGGATGCCTGGG 1108

Db        643 TTTTTGTTGTTGTTGTTTTTTGTTTGTTTGTTTTGGTGGGAGAGGGGAGGGATGCCTGGG 584

Qy       1109 AAGTGGTTAACAACTTTTTTCAAGTCACTTTACTAAACAAACTTTTGTAAATAGACCTTA 1168

Db        583 AAGTGGTTAACAACTTTTTTCAAGTCACTTTACTAAACAAACTCTTGTAAATAGACCTTA 524

Qy       1169 CCTTCTATTTTCGAGTTTCATTTATATTTTGCAGTGTAGCCAGCCTCATCAAAGAGCTGA 1228

Db        523 CCTTCTATTTTCGAGTTTCATTTATATTTTGCAGTGTMGCCMGCCTCMTCAAAGCGCTSA 464

Qy       1229 CTTACTCATTTGACTTTTGCACTGACTGTATTATCTGGGTATCTGCTGTGTCTGCACTTC 1288

Db        463 CTCACCCATTTGACTTTTGCACTGACTGTGTTATCTGGGTATCTGCTGTGTCTGCACTTC 404

Qy       1289 ATGGTAAACGGGATCTAAAATGCCTGGTGGCTTTTCACAAAAAGCAGATTTTCTTCATGT 1348

Db        403 ATGGTAAACGGGATCTAAAATGCCTGGTGGCTTTTCACAAAAAGCAGATTTTCTTCATGT 344

Qy       1349 ACTGTGATGTCTGATGCAATGCATCCTAGAACAAACTGGCCATTTGCTAGTTTACTCTAA 1408

Db        343 ACTGTGATGTCTGATGCAATGCATCCTAGAACAAACTGGCCATTTGCTAGTTTACTCTAA 284

Qy       1409 AGACTAAACATAGTCTTGGTGTGTGTGGTCTTACTCATCTTCTAGTACCTTTAAGGACAA 1468

Db        283 AGACTAAACATAGTCTTGGTGTGTGTGGTCTTACTCATCTTCTAGTACCTTTAAGGACAA 224

Qy       1469 ATCCTAAGGACTTGGACACTTGCAATAAAGAAATTTTATTTTAAACCCAAGCCTCCCTGG 1528

Db        223 ATCCTAAGGACTTGGACMCTTGCAATAAAGAAATTTTATTTTAAACCCAAGCCTCCCTGG 164

Qy       1529 ATTGATAATATATACACATTTGTCAGCATTTCCGGTCGTGGTGAGAGGCAGCTGTTTGAG 1588

Db        163 ATTGATAATATATACACATTTGTCAGCATTTCCGGTCGTGGTGAGAGGCAGCTGTTTGAG 104

Qy       1589 CTCCAATATGTGCAGCTTTGAACTAGGGCTGGGGTTGTGGGTGCCTCTTCTGAAAGGTCT 1648

Db        103 CTCCAATGTGTGCAGCTTTGAACTAGGGCTGGGGTTGTGGGTGCCTCTTCTGAAAGGTCT 44

Qy       1649 AACCAT-TATTGGATAACTGGCTTTTTTCTTCCTATGTCCT 1688

Db          43 AACCNTNNNTTGGNTNACTGGCTTTTTTCTTCCBCTTKSSK 3
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RESULT 3
AL537331
LOCUS AL537331 1201 bp mRNA linear EST 31-MAY-2003
DEFINITION AL537331 Homo sapiens FETAL BRAIN Homo sapiens cDNA clone CS0DF025YO05 5-PRIME, mRNA sequence.
ACCESSION AL537331
VERSION AL537331.2 GI:31261954
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 1201)
AUTHORS Li,W.B., Gruber,C., Jessee,J. and Polayes,D.
TITLE Full-length cDNA libraries and normalization
JOURNAL Unpublished (2001)
COMMENT On Feb 13, 2001 this sequence version replaced gi:12800824.
Contact: Genoscope
Genoscope - Centre National de Sequencage
BP 191 91006 EVRY cedex - France
Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr
Library was constructed by Life Technologies, a division of Invitrogen. This sequence belongs to sequence cluster 6242.f For more information about this cluster, see
http://www.genoscope.cns.fr/
cgi-bin/cluster.cgi?seq=CS0DF025AH03QP1&cluster=6242.f. Contact : Feng Liang Email : fliang@lifetech.com URL :
http://fulllength.invitrogen.com/ InVitroGen Corporation 1600 Faraday Avenue Genoscope sequence ID : CS0DF025AH03QP1.
FEATURES Location/Qualifiers
source 1. .1201
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="CS0DF025YO05"
/tissue_type="FETAL BRAIN"
/dev_stage="fetal"
/clone_lib="Homo sapiens FETAL BRAIN"
/note="Organ: brain; Vector: pCMVSPORT_6; 1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime end enriched, double-strand cDNA was digested with Not I and cloned into the Not I and EcoRV sites of the pCMVSPORT 6 vector. Library was not normalized."
ORIGIN

Query Match 53.9%; Score 931.2; DB 9; Length 1201;
Best Local Similarity 92.4%; Pred. No. 1.9e-166;
Matches 1051; Conservative 16; Mismatches 54; Indels 17; Gaps 8;

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Qy          3 GCCGGGTCCCAAGCCTGTGCCTGAGCCTGAGCCTGAGCCTGAGCCCGAGCCGGGAGCCGG 62

Db         76 GCCTGAGCCTGAGCCTGAGCCTGAGCCTGAGCCCGAGCCTGAGCCCGAGCCGGGAGCCGG 135

Qy         63 TCGCGGGGGCTCCGGGCTGTGGGACCGCTGGGCCCCCAGCGATGGCGACCCTGTGGGGAG 122

Db        136 TCGCGGGGGCTCCGGGCTGTGGGACCGCTGGGCCCCCAGCGATGGCGACCCTGTGGGGAG 195

Qy        123 GCCTTCTTCGGCTTGGCTCCTTGCTCAGCCTGTCGTGCCTGGCGCTTTCCGTGCTGCTGC 182

Db        196 GCCTTCTTCGGCTTGGCTCCTTGCTCAGCCTGTCGTGCCTGGCGCTTTCCGTGCTGCTGC 255

Qy        183 TGGCGCAGCTGTCAGACGCCGCCAAGAATTTCGAGGATGTCAGATGTAAATGTATCTGCC 242

Db        256 TGGCGCA-STGTCAGACGCCGCCAAGAATTTCGAGGATGTCAGATGTAAATGTATCTGCC 314

Qy        243 CTCCCTATAAAGAAAATTCTGGGCATATTTATAATAAGAACATATCTCAGAAAGATTGTG 302

Db        315 CTCCCTATAAAGAAAATTCTGGGCATATTTATAATAAGAACATATCTCAGAAAGATTGTG 374

Qy        303 ATTGCCTTCATGTTGTGGAGCCCATGCCTGTGCGGGGGCCTGATGTAGAAGCATACTGTC 362

Db        375 ATTGCCTTCATGTCGTGGAGCCCATGCCTGTGCGGGGGCCTGATGTAGAAGCATACTGTC 434

Qy        363 TACGCTGTGAATGCAAATATGAAGAAAGAAGCTCTGTCACAATCAAGGTTACCATTATAA 422

Db        435 TACGCTGTGAATGCAAATATGAAGAAAGAAGCTCTGTCACAATCAAGGTTACCATTATAA 494

Qy        423 TTTATCTCTCCATTTTGGGCCTTCTACTTCTGTACATGGTATATCTTACTCTGGTTGAGC 482

Db        495 TTTATCTCTCCATTTTGGGCCTTCTACTTCTGTACATGGTATATCTTACTCTGGTTGAGC 554

Qy        483 CCATACTGAAGAGGCGCCTCTTTGGACATGCACAGTTGATACAGAGTGATGATGATATTG 542
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Db        555 CCATACTGAAGAGGCGCCTCTTTGGACATGCACAGTTGATACAGAGTGATGATGATATTG 614

Qy        543 GGGATCACCAGCCTTTTGCAAATGCACACGATGTGCTAGCCCGCTCCCGCAGTCGAGCCA 602

Db        615 GGGATCACCAGCCTTTTGCAAATGCACACGATGTGCTAGCCCGCTCCCGCAGTCGAGCCA 674

Qy        603 ACGTGCTGAACAAGGTAGAATATGCACAGCAGCGCTGGAAGCTTCAAGTCCAAGAGCAGC 662

Db        675 ACGTGCTGAACAAGGTAGAATATGCACAGCAGCGCTGGAAGCTTCAAGTCCAAGAGCAGC 734

Qy        663 GAAAGTCTGTCTTTGACCGGCATGTTGTCCTCAGCTAATTGGGAATTGAATTCAAGGTGA 722

Db        735 GAAAGTCTGTCTTTGACCGGCATGTTGTCCTCAGCTAATTGGGAATTGAATTCAAGGTGA 794

Qy        723 CTAGAAAGAAACAGGCAGACAACTGGAAAGAACTGACTGGGTTTTGCTGGGTTTCATTTT 782

Db        795 CTAGAAAGAAACAGGCAGACAACTGGAAAGAACTGACTGGGTTTTGCTGGGTTTCATTTT 854

Qy        783 AATACCTTGTTGATTTCACCAACTGTTGCTGGAAGATTCAAAACTGGAAGCAAAAACTTG 842

Db        855 AATACCTTGTTGATTTCACCAACTGTTGCTGGAAGATTCAAAACTGGAAGCAAAAACTTG 914

Qy        843 CTTGA-TTTTTTTTTCTTGTTAACGTAATAATAGAGACATTTTTAAAAGCACACAGCTCA 901

Db        915 CTTGATTTTTTTTTTCTTGTTAACGTAATAATAGAGACATTTTTAAAA-CACACAGCTCA 973

Qy        902 AAGTCAGCCAATAAGTCTTTTCCTATTTGTGACTTTTACTAATAAAAATAAATCTGCCTG 961

Db        974 AAGTCAGCCAATAAGTCTTTTCYTATTTGTGACTTTTACTAAT-AAAAWAAATCTGCCTG 1032

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Db       1033 TAAATTATYTKG-AGTCCTTTACTKGGACAAGCMYCTCTTTTY----CCACATAGTTTAA 1087

Qy       1022 ACTTGACTTTCAAGATAATTTTCAGGGTTTTTGTTGTTGTTGTTTTTTGTTTGTTTGTTT 1081

Db       1088 MTTGRCTTTCAGA---WAWTTTCAGGGT-----TTGGTGGTGKTGTTTTTTTTKTTGTTT 1139

Qy       1082 TGGTGGGAGAGGGGAGGGATGCCTGGGAAGTGGTTAACAACTTTTTTCAAGTCACTTT 1139

Db       1140 TGTGGGGAGGGGGGGWGCCGGGAAKGGTAAMACTTTTCAAKCAYTTACAAAMAATTTT 1197


RESULT 4
BX425270
LOCUS       BX425270               1201 bp    mRNA    linear   EST 15-MAY-2003
DEFINITION  BX425270 Homo sapiens NEUROBLASTOMA Homo sapiens cDNA clone
            CL0BB007ZA11 5-PRIME, mRNA sequence.
ACCESSION   BX425270
VERSION     BX425270.1  GI:30778450
KEYWORDS    EST.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 1201)
  AUTHORS   Li,W.B., Gruber,C., Jessee,J. and Polayes,D.
  TITLE     Full-length cDNA libraries and normalization
  JOURNAL   Unpublished (2001)
COMMENT     Contact: Genoscope
            Genoscope - Centre National de Sequencage
            BP 191 91006 EVRY cedex - France
            Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr
            Library was constructed by Life Technologies, a division of
            Invitrogen. This sequence belongs to sequence cluster 6242.f For
            more information about this cluster, see
            http://www.genoscope.cns.fr/
            cgi-bin/cluster.cgi?seq=CL0BB007ZA11RP1&cluster=6242.f. Contact :
            Feng Liang Email : fliang@lifetech.com URL :
            http://fulllength.invitrogen.com/ InVitroGen Corporation 1600
            Faraday Avenue Genoscope sequence ID : CL0BB007ZA11RP1.
FEATURES             Location/Qualifiers
     source          1. .1201
                     /organism="Homo sapiens"
                     /mol_type="mRNA"
                     /db_xref="taxon:9606"
                     /clone="CL0BB007ZA11"
                     /tissue_type="NEUROBLASTOMA"
                     /clone_lib="Homo sapiens NEUROBLASTOMA"
                     /note="Vector: pCMVSPORT_6; 1st strand cDNA was primed
                     with a NotI-oligo(dT) primer. Five prime end enriched,
                     double-strand cDNA was digested with Not I and cloned into
                     the Not I and EcoRV sites of the pCMVSPORT 6 vector.
                     Library was not normalized."
ORIGIN

  Query Match             53.9%;  Score 931.2;  DB 13;  Length 1201;
  Best Local Similarity   93.6%;  Pred. No. 1.9e-166;
  Matches 1050;  Conservative   16;  Mismatches   45;  Indels   11;  Gaps    9;

Qy          7 GGTCCCAAGCCTGTGCCTGAGCCTGAGCCTGAGCCTGAGCCCGAGCCGGGAGCCGGTCGC 66

Db         37 GGGCCCAAGCCTGTGCCTGAGCCTGAGCCTGAGCCTGAGCCCGAGCCGGGAGCCGGTCGC 96

Qy         67 GGGGGCTCCGGGCTGTG-GGACCGCTGGGCCCCCAGCGATGGCGACCCTGTGGGGAGGCC 125

Db         97 GGGGGCTCCGGGCTGTGAGGACCGCTGGGCCCCCAGCGATGGCGACCCTGTGGGGAGGCC 156

Qy        126 TTCTTCGGCTTGGCTCCTTGCTCAGCCTGTCGTGCCTGGCGCTTTCCGTG-CTGCTGCT- 183

Db        157 TTCTTCGGCTTGGCTCCTTGCTCAGCCTGTCGTGCCTGGCGCTTTCCGTGACTGCTGCTA 216

Qy        184 GGCGCAGCTGTCAGACGCCGCCAAGAATTTCGAGGATGTCAGATGTAAATGTATCTGCCC 243

Db        217 GGCGCASTGGTCAGACGCCGCCAAGAATTTCGAGGATGTCAGATGTAAATGTATCTGCCC 276

Qy        244 TCCCTATAAAGAAAATTCTGGGCATATTTATAATAAGAACATATCTCAGAAAGATTGTGA 303

Db        277 TCCCTATAAAGAAAATTCTGGGCATATTTATAATAAGAACATATCTCAGAAAGATTGTGA 336

Qy        304 TTGCCTTCATGTTGT-GGAGCCCATGCCTGTGCGGGGGCCTGATGTAGAAGCATACTGTC 362

Db        337 TTGCCTTCATGTTGTAGGAGCCCATGCCTGTGCGGGGGCCTGATGTAGAAGCATACTGTC 396

Qy        363 TACGCTGTGAATGCAAATATGAAGAAAGAAGCTCTGTCACAATCAAGGTTACCATTATAA 422

Db        397 TACGCTGTGAATGCAAATATGAAGAAAGAAGCTCTGTCACAATCAAGGTTACCATTATAA 456

Qy        423 TTTATCTCTCCATTTTGGGCCTTCTACTTCTGTACATGGTATATCTTACTCTGGTTGAGC 482

Db        457 TTTATCTCTCCATTTTGGGCCTTCTACTTCTGTACATGGTATATCTTACTCTGGTTGAGC 516

Qy        483 CCATACTGAAGAGGCGCCTCTTTGGACATGCACAGTTGATACAGAGTGATGATGATATTG 542

Db        517 CCATACTGAAGAGGCGCCTCTTTGGACATGCACAGTTGATACAGAGTGATGATGATATTG 576

Qy        543 GGGATCACCAGCCTTTTGCAAATGCACACGATGTGCTAGCCCGCTCCCGCAGTCGAGCCA 602

Db        577 GGGATCACCAGCCTTTTGCAAATGCACACGATGTGCTAGCCCGCTCCCGCAGTCGAGCCA 636

Qy        603 ACGTGCTGAACAAGGTAGAATATGCACAGCAGCGCTGGAAGCTTCAAGTCCAAGAGCAGC 662

Db        637 ACGTGCTGAACAAGGTAGAATATGCACAGCAGCGCTGGAAGCTTCAAGTCCAAGAGCAGC 696

Qy        663 GAAAGTCTGTCTTTGACCGGCATGTTGTCCTCAGCTAATTGGGAATTGAATTCAAGGTGA 722

Db        697 GAAAGTCTGTCTTTGACCGGCATGTTGTCCTCAGCTAATTGGGAATTGAATTCAAGGTGA 756

Qy        723 CTAGAAAGAAACAGGCAGACAACTGGAAAGAACTGACTGGGTTTTGCTGGGTTTCATTTT 782

Db        757 CTAGAAAGAAACAGGCAGACAACTGGAAAGAACTGACTGGGTTTTGCTGGGTTTCATTTT 816

Qy        783 AATACCTTGTTGATTTCACCAACTGTTGCTGGAAGATTCAAAACTGGAAGCAAAAACTTG 842

Db        817 AATACCTTGTTGATTTCACCAACTGTTGCTGGAAGATTCAAAACTGGAAGCAAAAACTTG 876
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Qy        843 CTTGATTTTTTTTTCTTGTTAACGTAATAATAGAGACATTTTTAAAAGCACACAGCTCAA 902
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Db        877 CTTGATTTTTTTTTCTTGTTAACGTAATAATAGAGAMATTTTTAAAAGCACACAGCTCAA 936

Qy        903 AGTCAGCCAATAAGTCTTTTCCTATTTGTGACTTTTACTAATAAAAATAAATCTGCCTGT 962
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Db        937 AGTCAGCCAATAAGTCTTTTCCTATTTGTGACTTT--ACTAATAAAAWWAATCTGCCTGT 994

Qy        963 AAATTATCTTGAAGTCCTTTACCTGGAACAAGCACTCTCTTTTTCACCACATAGTTTTAA 1022
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Db        995 AAATTATCTTG-ARTCCTTTACCTGG-AMAAGCACTCTCTTTTTCACACM--TAGTTTAA 1050

Qy       1023 CTTGACTTTCAAGATAATTTTCAGGGTTTTTGTTGTTGTTGTTTTTTGTTTGTTTGTTTT 1082
              |||||||||| |||:|:|||   || |||:|  |  |:|| |||||||||: ||||
Db       1051 CTTGACTTTC-AGAWAWTTTMAGGGTTTTKTTGTTGTKTTTTTTTTTGTTKTTTTGGCGG 1109

Qy       1083 GGTGGGAGAGGGGAGGGATGCCTGGGAAGTGGTTAACAACTT 1124
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Db       1110 GGAGGGGGGGGTGCYGGGGAGKGKTAAAACTTTTHAWATAMTT 1151
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RESULT 5
AL562476/c
LOCUS AL562476 1201 bp mRNA linear EST 31-MAY-2003
DEFINITION AL562476 Homo sapiens NEUROBLASTOMA COT 25-NORMALIZED Homo sapiens cDNA clone CS0DC011YH24 3-PRIME, mRNA sequence.
ACCESSION AL562476
VERSION AL562476.2 GI:31286488
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 1201)
AUTHORS Li,W.B., Gruber,C., Jessee,J. and Polayes,D.
TITLE Full-length cDNA libraries and normalization
JOURNAL Unpublished (2001)
COMMENT On Feb 15, 2001 this sequence version replaced gi:12910933.
Contact: Genoscope
Genoscope - Centre National de Sequencage
BP 191 91006 EVRY cedex - France
Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr
Library was constructed by Life Technologies, a division of Invitrogen. This sequence belongs to sequence cluster 6173.r
Contact : Feng Liang Email : fliang@lifetech.com URL : http://fulllength.invitrogen.com/ InVitroGen Corporation 1600 Faraday Avenue Genoscope sequence ID : CS0DC011DD12NP1.
FEATURES Location/Qualifiers
source 1. .1201
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="CS0DC011YH24"
/tissue_type="NEUROBLASTOMA COT 25-NORMALIZED"
/clone_lib="Homo sapiens NEUROBLASTOMA COT 25-NORMALIZED"
/note="1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime end enriched, double-strand cDNA was digested with Not I and cloned into the Not I and EcoR V sites of the pCMVSPORT 6 vector. Library was normalized."
ORIGIN

Query Match 52.9%; Score 913.8; DB 9; Length 1201;
Best Local Similarity 91.0%; Pred. No. 3.8e-163;
Matches 935; Conservative 33; Mismatches 56; Indels 3; Gaps 2;

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Qy        670 TGTCTTTGACCGGCATGTTGTCCTCAGCTAATTGGGAATTGAATTCAAGGTGACTAGAAA 729
              | | | |   | |:   :||:||||||||||:||  | |  | |::|||||||||||||
Db       1025 TCTKTCTTGACCGSCATKTGYCCTCAGCTAATKGG--AATTGAATYMAGGTGACTAGAAA 968

Qy        730 GAAACAGGCAGACAACTGGAAAGAACTGACTGGGTTTTGCTGGGTTTCATTTTAATACCT 789
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        967 GAAACAGGCAGACAACTGGAAAGAACTGACTGGGTTTTGCTGGGTTTCATTTTAATACCT 908

Qy        790 TGTTGATTTCACCAACTGTTGCTGGAAGATTCAAAACTGGAAGCAAAAACTTGCTTGATT 849
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        907 TGTTGATTTCACCAACTGTTGCTGGAAGATTCAAAACTGGAAGCAAAAACTTGCTTGATT 848

Qy        850 TTTTTTTCTTGTTAACGTAATAATAGAGACATTTTTAAAAGCACACAGCTCAAAGTCAGC 909
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Db        847 TTTTTCTCTTGTTAACGTAATAATAGAGACATTTTTAAAAGCACACAGCTCAAAGTCAGC 788

Qy        910 CAATAAGTCTTTTCCTATTTGTGACTTTTACTAATAAAAATAAATCTGCCTGTAAATTAT 969
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Db        787 CAATAAGTCTTTTCCTATTTGTGACTTTTACTAATAAAAATAAATCTGCCTGTAAATTAT 728

Qy        970 CTTGAAGTCCTTTACCTGGAACAAGCACTCTCTTTTTCACCACATAGTTTTAACTTGACT 1029
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Db        727 CTTGAAGTCCTTTACCTGGAACAAGCACTCTCTTTTTCACCACATAGTTTTAACTTGACT 668

Qy       1030 TTCAAGATAATTTTCAGGGTTTTTGTTGTTGTTGTTTTTTGTTTGTTTGTTTTGGTGGGA 1089
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Db        667 TTCAAGATAATTTTCAGGGTTTTTGTTGTTGTTGTTTTTNGTTTGTTTGTTTTGGNGGGA 608

Qy       1090 GAGGGGAGGGATGCCTGGGAAGTGGTTAACAACTTTTTTCAAGTCACTTTACTAAACAAA 1149
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Db        607 GAGGGGAGGGANGCCTGGGAAGTGGTTAACAACTTTTTTCAAGTCACTTTACTAAACAAA 548

Qy       1150 CTTTTGTAAATAGACCTTACCTTCTATTTTCGAGTTTCATTTATATTTTGCAGTGTAGCC 1209
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Db        547 CTTTTGTAAATAGACCTTACCTTCTATTTTCGAGTYTCATTTATATTTTGCAGTGTAGCC 488

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Db        487 AGCCTCATCAAAGAGCTCACTCACTCATTTSACTTTTGCACTGACTGTATTATCTGGGTA 428

Qy       1270 TCTGCTGTGTCTGCACTTCATGGTAAACGGGATCTAAAATGCCTGGTGGCTTTTCACAAA 1329
              ||  |||||||||||||||||||||||||||||||||:::|||||||||||||||||||||
Db        427 TCMGCTGTGTCTGCACTTCATGGTAAACGGGATCYMMAATGCCTGGTGGCTTTTCACAAA 368

Qy       1330 AAGCAGATTTTCTTCATGTACTGTGATGTCTGATGCAATGCATCCTAGAACAAACTGGCC 1389
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Db        367 AAGCASATTTTCTYCATGTACYGTGATGTCTGATGCAATGCATCCTAGAACAMACTGGCC 308

Qy       1390 ATTTGCTAGTTTACTCTAAAGACTAAACATAGTCTTGGTGTGTGTGGTCTTACTCATCTT 1449
              ||||||||||||||||:||:::|||||||||||||||||||||||:|||||||||||||
Db        307 ATTTGCTAGTTTACTCYAAMSMCTAAACATAGTCTTGGTGTGTGTGGSTCTTACTCATCTT 248

Qy       1450 CTAGTACCTTTAAGGACAAATCCTAAGGACTTGGACACTTGCAATAAAGAAATTTTATTT 1509
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Db        247 CTAGTMCCTTTAAGGACAAATCCTAAGCACTTGGACMCYYSCAATAAMSMAATTTTATTT 188

Qy       1510 TAAACCCAAGCCTCCCTGGATTGATAATATATACACATTTGTCAGCATTTCCGGTCGTGG 1569
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Qy       1570 TGAGAGGCAGCTGTTTGAGCTCCAATATGTGCAGCTTTGAACTAGGGCTGGGGTTGTGGG 1629
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Db        127 NNAGACNCACCTNNNNCANCCCCAATNNNNNCANCTNNGAACTAGGGCTGGGGTTGTGGG 68

Qy       1630 TGCCTCTTCTGAAAGGTCTAACCATTATTGGATAAC-TGGCTTTTTTCTTCCTATGTCCT 1688
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Db          67 TGCCTCTTCTGAAAGGTCTAACCATTATTGGATAACNTGCNTTTTTTCTCCCTCTSTCCT 8

Qy       1689 CTTTGGA 1695
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RESULT 6
BX440898
LOCUS BX440898 1201 bp mRNA linear EST 15-MAY-2003
DEFINITION BX440898 Homo sapiens FETAL BRAIN Homo sapiens cDNA clone CS0DF012YE14 5-PRIME, mRNA sequence.
ACCESSION BX440898
VERSION BX440898.1 GI:30775890
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KEYWORDS    EST.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 1201)
  AUTHORS   Li,W.B., Gruber,C., Jessee,J. and Polayes,D.
  TITLE     Full-length cDNA libraries and normalization
  JOURNAL   Unpublished (2001)
COMMENT     Contact: Genoscope
            Genoscope - Centre National de Sequencage
            BP 191 91006 EVRY cedex - France
            Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr
            Library was constructed by Life Technologies, a division of
            Invitrogen. This sequence belongs to sequence cluster 6242.f For
            more information about this cluster, see
            http://www.genoscope.cns.fr/
            cgi-bin/cluster.cgi?seq=CS0DF012BC07QP1&cluster=6242.f. Contact :
            Feng Liang Email : fliang@lifetech.com URL :
            http://fulllength.invitrogen.com/ InVitroGen Corporation 1600
            Faraday Avenue Genoscope sequence ID : CS0DF012BC07QP1.
FEATURES             Location/Qualifiers
     source          1. .1201
                     /organism="Homo sapiens"
                     /mol_type="mRNA"
                     /db_xref="taxon:9606"
                     /clone="CS0DF012YE14"
                     /tissue_type="FETAL BRAIN"
                     /dev_stage="fetal"
                     /clone_lib="Homo sapiens FETAL BRAIN"
                     /note="Organ: brain; Vector: pCMVSPORT_6; 1st strand cDNA
                     was primed with a NotI-oligo(dT) primer. Five prime end
                     enriched, double-strand cDNA was digested with Not I and
                     cloned into the Not I and EcoRV sites of the pCMVSPORT 6
                     vector. Library was not normalized."
ORIGIN

  Query Match             52.3%;  Score 904;  DB 13;  Length 1201;
  Best Local Similarity   93.8%;  Pred. No. 2.7e-161;
  Matches  951;  Conservative   20;  Mismatches   36;  Indels    7;  Gaps    3;

Qy        113 CTGTGGGGAGGCCTTCTTCGGCTTGGCTCCTTGCTCAGCCTGTCGTGCCTGGCGCTTTCC 172
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Db         61 CTGTGGGGAGGCCTTCTTCGGCTTGGCTCCTTGCTCAGCCTGTCGTGCCTGGCGCTTTCC 120

Qy        173 GTGCTGCTGCTGGCGCAGCTGTCAGACGCCGCCAAGAATTTCGAGGATGTCAGATGTAAA 232
              |||||||||||||||| :|||||||||||||||||||||||||||||||||||||||||
Db        121 GTGCTGCTGCTGGCGCA-STGTCAGACGCCGCCAAGAATTTCGAGGATGTCAGATGTAAA 179

Qy        233 TGTATCTGCCCTCCCTATAAAGAAAATTCTGGGCATATTTATAATAAGAACATATCTCAG 292
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Db        180 TGTATCTGCCCTCCCTATAAAGAAAATTCTGGGCATATTTATAATAAGAACATATCTCAG 239

Qy        293 AAAGATTGTGATTGCCTTCATGTTGTGGAGCCCATGCCTGTGCGGGGGCCTGATGTAGAA 352
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        240 AAAGATTGTGATTGCCTTCATGTTGTGGAGCCCATGCCTGTGCGGGGGCCTGATGTAGAA 299

Qy        353 GCATACTGTCTACGCTGTGAATGCAAATATGAAGAAAGAAGCTCTGTCACAATCAAGGTT 412
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Db        300 GCATACTGTCTACGCTGTGAATGCAAATATGAAGAAAGAAGCTCTGTCACAATCAAGGTT 359

Qy        413 ACCATTATAATTTATCTCTCCATTTTGGGCCTTCTACTTCTGTACATGGTATATCTTACT 472
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Db        360 ACCATTATAATTTATCTCTCCATTTTGGGCCTTCTACTTCTGTACATGGTATATCTTACT 419

Qy        473 CTGGTTGAGCCCATACTGAAGAGGCGCCTCTTTGGACATGCACAGTTGATACAGAGTGAT 532
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Db        420 CTGGTTGAGCCCATACTGAAGAGGCGCCTCTTTGGACATGCACAGTTGATACAGAGTGAT 479

Qy        533 GATGATATTGGGGATCACCAGCCTTTTGCAAATGCACACGATGTGCTAGCCCGCTCCCGC 592
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Qy        593 AGTCGAGCCAACGTGCTGAACAAGGTAGAATATGCACAGCAGCGCTGGAAGCTTCAAGTC 652
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Db        540 AGTCGAGCCAACGTGCTGAACAAGGTAGAATATGCACAGCAGCGCTGGAAGCTTCAAGTC 599

Qy        653 CAAGAGCAGCGAAAGTCTGTCTTTGACCGGCATGTTGTCCTCAGCTAATTGGGAATTGAA 712
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Db        600 CAAGAGCAGCGAAAGTCTGTCTTTGACCGGCATGTTGTCCTCAGCTAATTGGGAATTGAA 659

Qy        713 TTCAAGGTGACTAGAAAGAAACAGGCAGACAACTGGAAAGAACTGACTGGGTTTTGCTGG 772
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Qy        773 GTTTCATTTTAATACCTTGTTGATTTCACCAACTGTTGCTGGAAGATTCAAAACTGGAAG 832
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Db        720 GTTTCATTTTAATACCTTGTTGATTTCACCAACTGTTGCTGGAAGATTCAAAACTGGAAG 779

Qy        833 CAAAAACTTGCTTGATTTTTTTTTCTTGTTAACGTAATAATAGAGACATTTTTAAAAGCA 892
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Db        780 CAAAAACTTGCTTGATTTTTTTTTCTTGTTAACGTAATAATAGAGACATTTTTAAAAGCA 839

Qy        893 CACAGCTCAAAGTCAGCCAATAAGTCTTTTCCTATTTGTGACTTTTACTAATAAAAATAA 952
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Qy        953 ATCTGCCTGTAAATTATCTTGAAGTCCTTTACCTGGAACAAGCACTCTCTTTTTCACCAC 1012
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Qy       1073 TGTTTGTTTTGGTGGGAGAGGGGAGGGATGCCTGGGAAGTGGTTAACAACTTTT 1126
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Db       1019 GGGTTTT-----TGGBGSMRRGGGRGGGAKSCYKGGRAGKGGTWAMAMKTTTTY 1067


RESULT 7
AL550557/c
LOCUS       AL550557               1201 bp    mRNA    linear   EST 31-MAY-2003
DEFINITION  AL550557 Homo sapiens PLACENTA COT 25-NORMALIZED Homo sapiens cDNA
            clone CS0DI058YJ16 3-PRIME, mRNA sequence.
ACCESSION   AL550557
VERSION     AL550557.2  GI:31272374
KEYWORDS    EST.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 1201)
  AUTHORS   Li,W.B., Gruber,C., Jessee,J. and Polayes,D.
  TITLE     Full-length cDNA libraries and normalization
  JOURNAL   Unpublished (2001)
COMMENT     On Feb 15, 2001 this sequence version replaced gi:12887637.
            Contact: Genoscope
            Genoscope - Centre National de Sequencage
            BP 191 91006 EVRY cedex - France
            Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr
            Library was constructed by Life Technologies, a division of
            Invitrogen. This sequence belongs to sequence cluster 6173.r
            Contact : Feng Liang Email : fliang@lifetech.com URL :
            http://fulllength.invitrogen.com/ InVitroGen Corporation 1600
            Faraday Avenue Genoscope sequence ID : CS0DI058DE08NP1.
FEATURES             Location/Qualifiers
     source          1. .1201
                     /organism="Homo sapiens"
                     /mol_type="mRNA"
                     /db_xref="taxon:9606"
                     /clone="CS0DI058YJ16"
                     /tissue_type="PLACENTA COT 25-NORMALIZED"
                     /clone_lib="Homo sapiens PLACENTA COT 25-NORMALIZED"
                     /note="1st strand cDNA was primed with a NotI-oligo(dT)
                     primer. Five prime end enriched, double-strand cDNA was
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digested with Not I and cloned into the Not I and EcoR V sites of the pCMVSPORT 6 vector. Library was normalized."

ORIGIN

Query Match 52.3%; Score 903.4; DB 9; Length 1201;
Best Local Similarity 95.9%; Pred. No. 3.5e-161;
Matches 963; Conservative 7; Mismatches 24; Indels 10; Gaps 4;

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Qy       482 CCCATACTGAAGAGGCGCCTCTTTGGACATGCACAGTTGATACAGAGTGATGATGATATT 541
            :|||||||||||| |||||||||||           :  | | || |::|||||     |
Db      1012 SCCATACTGAAGA-GCGCCTCTTTGACATGCACAKTKATACAGAGTGWKATGAT----AT 958

Qy       542 GGGGATCACCAGCCTTTTGCAAATGCACACGATGTGCTAGCCCGCTCCCGCAGTCGAGCC 601
            |||||||||||||| ||||||||||||||||||||||||||:|||||||||||||||||
Db       957 GGGGATCACCAGCC-TTTGCAAATGCACACGATGTGCTAGCCCSCTCCCGCAGTCGAGCC 899

Qy       602 AACGTGCTGAACAAGGTAGAATATGCACAGCAGCGCTGGAAGCTTCAAGTCCAAGAGCAG 661
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       898 AACGTGCTGAACAAGGTAGAATATGCACAGCAGCGCTGGAAGCTTCAAGTCCAAGAGCAG 839

Qy       662 CGAAAGTCTGTCTTTGACCGGCATGTTGTCCTCAGCTAATTGGGAATTGAATTCAAGGTG 721
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Db       838 CGAAAGTCTGTCTTTGACCGGCATGTTGTCCTCAGCTAATTGGGAATTGAATTCAAGGTG 779

Qy       722 ACTAGAAAGAAACAGGCAGACAACTGGAAAGAACTGACTGGGTTTTGCTGGGTTTCATTT 781
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Qy       782 TAATACCTTGTTGATTTCACCAACTGTTGCTGGAAGATTCAAAACTGGAAGCAAAAACTT 841
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Qy       842 GCTTGATTTTTTTTTCTTGTTAACGTAATAATAGAGACATTTTTAAAAGCACACAGCTCA 901
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Db       658 GCTTGATTTTTTTTTCTTGTTAACGTAATAATAGAGACATTTTTAAAAGCACACAGCTCA 599

Qy       902 AAGTCAGCCAATAAGTCTTTTCCTATTTGTGACTTTTACTAATAAAAATAAATCTGCCTG 961
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Db       598 AAGTCAGCCAATAAGTCTTTTCCTATTTGTGACTTTTACTAATAAAAATAAATCTGCCTG 539

Qy       962 TAAATTATCTTGAAGTCCTTTACCTGGAACAAGCACTCTCTTTTTCACCACATAGTTTTA 1021
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Qy      1022 ACTTGACTTTCAAGATAATTTTCAGGGTTTTTGTTGTTGTTGTTTTTTGTTTGTTTGTTT 1081
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Db       478 ACTTGACTTTCAAGATAATTTTCAGGGTTTTTGTTGTTGTTGTTTTTTGTTTGTTTGTTT 419

Qy      1082 TGGTGGGAGAGGGGAGGGATGCCTGGGAAGTGGTTAACAACTTTTTTCAAGTCACTTTAC 1141
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Qy      1322 TTCACAAAAAGCAGATTTTCTTCATGTACTGTGATGTCTGATGCAATGCATCCTAGAACA 1381
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Qy      1382 ----AACTGGCCATTTGCTAGTTTACTCTAAAGACTAAACATAGTCTTGGTGTGTGTGGT 1437
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RESULT 8
AK077253
LOCUS AK077253 1642 bp mRNA linear HTC 18-SEP-2003
DEFINITION Mus musculus 11 days pregnant adult female ovary and uterus cDNA, RIKEN full-length enriched library, clone:5031426I03 product:C11ORF15 PROTEIN homolog [Homo sapiens], full insert sequence.
ACCESSION AK077253
VERSION AK077253.1 GI:26346117
KEYWORDS HTC; CAP trapper.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE 1
AUTHORS Carninci,P. and Hayashizaki,Y.
TITLE High-efficiency full-length cDNA cloning
JOURNAL Meth. Enzymol. 303, 19-44 (1999)
MEDLINE 99279253
PUBMED 10349636
REFERENCE 2
AUTHORS Carninci,P., Shibata,Y., Hayatsu,N., Sugahara,Y., Shibata,K., Itoh,M., Konno,H., Okazaki,Y., Muramatsu,M. and Hayashizaki,Y.
TITLE Normalization and subtraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new genes
JOURNAL Genome Res. 10 (10), 1617-1630 (2000)
MEDLINE 20499374
PUBMED 11042159
REFERENCE 3
AUTHORS Shibata,K., Itoh,M., Aizawa,K., Nagaoka,S., Sasaki,N., Carninci,P., Konno,H., Akiyama,J., Nishi,K., Kitsunai,T., Tashiro,H., Itoh,M., Sumi,N., Ishii,Y., Nakamura,S., Hazama,M., Nishine,T., Harada,A., Yamamoto,R., Matsumoto,H., Sakaguchi,S., Ikegami,T., Kashiwagi,K., Fujiwake,S., Inoue,K., Togawa,Y., Izawa,M., Ohara,E., Watahiki,M., Yoneda,Y., Ishikawa,T., Ozawa,K., Tanaka,T., Matsuura,S., Kawai,J., Okazaki,Y., Muramatsu,M., Inoue,Y., Kira,A. and Hayashizaki,Y.
TITLE RIKEN integrated sequence analysis (RISA) system--384-format sequencing pipeline with 384 multicapillary sequencer
JOURNAL Genome Res. 10 (11), 1757-1771 (2000)
MEDLINE 20530913
PUBMED 11076861
REFERENCE 4
AUTHORS The RIKEN Genome Exploration Research Group Phase II Team and the FANTOM Consortium.
TITLE Functional annotation of a full-length mouse cDNA collection
JOURNAL Nature 409, 685-690 (2001)
REFERENCE 5
AUTHORS The FANTOM Consortium and the RIKEN Genome Exploration Research Group Phase I & II Team.
TITLE Analysis of the mouse transcriptome based on functional annotation of 60,770 full-length cDNAs
JOURNAL Nature 420, 563-573 (2002)
REFERENCE 6 (bases 1 to 1642)
AUTHORS Adachi,J., Aizawa,K., Akimura,T., Arakawa,T., Bono,H., Carninci,P., Fukuda,S., Furuno,M., Hanagaki,T., Hara,A., Hashizume,W., Hayashida,K., Hayatsu,N., Hiramoto,K., Hiraoka,T., Hirozane,T., Hori,F., Imotani,K., Ishii,Y., Itoh,M., Kagawa,I., Kasukawa,T., Katoh,H., Kawai,J., Kojima,Y., Kondo,S., Konno,H., Kouda,M., Koya,S., Kurihara,C., Matsuyama,T., Miyazaki,A., Murata,M., Nakamura,M., Nishi,K., Nomura,K., Numazaki,R., Ohno,M., Ohsato,N., Okazaki,Y., Saito,R., Saitoh,H., Sakai,C., Sakai,K., Sakazume,N., Sano,H., Sasaki,D., Shibata,K., Shinagawa,A., Shiraki,T., Sogabe,Y., Tagami,M., Tagawa,A., Takahashi,F., Takaku-Akahira,S., Takeda,Y., Tanaka,T., Tomaru,A., Toya,T., Yasunishi,A., Muramatsu,M. and Hayashizaki,Y.
TITLE Direct Submission
JOURNAL Submitted (16-APR-2002) Yoshihide Hayashizaki, The Institute of Physical and Chemical Research (RIKEN), Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center (GSC),

```
            RIKEN Yokohama Institute; 1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama,
            Kanagawa 230-0045, Japan (E-mail:genome-res@gsc.riken.go.jp,
            URL:http://genome.gsc.riken.go.jp/, Tel:81-45-503-9222,
            Fax:81-45-503-9216)
COMMENT     cDNA library was prepared and sequenced in Mouse Genome
            Encyclopedia Project of Genome Exploration Research Group in Riken
            Genomic Sciences Center and Genome Science Laboratory in RIKEN.
            Division of Experimental Animal Research in Riken contributed to
            prepare mouse tissues.
            Please visit our web site for further details.
            URL:http://genome.gsc.riken.go.jp/
            URL:http://fantom.gsc.riken.go.jp/.
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     polyA_site       1642
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Qy         68 GGGGCTCCGGGCTGTGGGACCGCTGGGCCCCCAGCGATGGCGACCCT---GTGGGGAGGC 124
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Db          6 GGGGCTCGGGGCTCGCAGGAGCGGCTGGCTCCCGCGATGGCGAGCCTATGGTGCGGAAAC 65

Qy        125 CTTCTTCGGCTTGGCTCCTTGCTCAGCCTGTCGTGCCTGGCGCTTTCCGTGCTGCTGCTG 184
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Db         66 CTGCTGCGGCTGGGCTCGGGGCTCAGCATGTCCTGCCTGGCGCTGTCGGTGCTGCTGCTC 125

Qy        185 GCGCAGCTGTCAGACGCCGCCAAGAATTTCGAGGATGTCAGATGTAAATGTATCTGCCCT 244
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Db        126 GCGCAGCTGACAGGCGCCGCCAAGAATTTTGAAGATGTGAGATGTAAATGCATCTGCCCT 185

Qy        245 CCCTATAAAGAAAATTCTGGGCATATTTATAATAAGAACATATCTCAGAAAGATTGTGAT 304
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Db        186 CCCTATAAAGAGAATCCTGGGCACATTTATAATAAGAATATATCTCAGAAAGATTGTGAT 245

Qy        305 TGCCTTCATGTTGTGGAGCCCATGCCTGTGCGGGGGCCTGATGTAGAAGCATACTGTCTA 364
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Qy        365 CGCTGTGAATGCAAATATGAAGAAAGAAGCTCTGTCACAATCAAGGTTACCATTATAATT 424
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Db        306 CGCTGTGAATGCAAATACGAAGAGAGAAGCTCTGTCACAATCAAGGTTACCATTATAATT 365

Qy        425 TATCTCTCCATTTTGGGCCTTCTACTTCTGTACATGGTATATCTTACTCTGGTTGAGCCC 484
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Db        366 TATCTCTCTATTTTGGGCCTTCTGCTTCTGTACATGGTATATCTTACCTTAGTTGAGCCC 425

Qy        485 ATACTGAAGAGGCGCCTCTTTGGACATGCACAGTTGATACAGAGTGATGATGATATTGGG 544
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Qy        545 GATCACCAGCCTTTTGCAAATGCACACGATGTGCTAGCCCGCTCCCGCAGTCGAGCCAAC 604
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Qy        665 AAGTCTGTCTTTGACCGGCATGTTGTCCTCAGCTAATTGGGAATTGAATTCAAGGTGACT 724
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Qy        725 AGAAAGAAACAGGCAGACAACTGGAAAGAACTGACTGGGTTTTGCTGGGTTTCATT---T 781
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Db        665 AGGAAG-AACACGCAGACAACTGGGAAGAATTGTCTGGGTGTCCGTGCGTTTTAATGCCA 723

Qy        782 TAATACCTTGTTGATTTCACCAACTGTTGCTGGAAGATTCAAAACTGGAAGCAAAAACTT 841
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Qy        842 GCTTGATTTTTTTTTCTTGTTAACGTAATAATAGAGACATTTTTAAAAGCACACAGCTCA 901
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Qy        962 TAAATTATCTTGAAGTCCTTTACCTGGAACAAGCACTCTCTTTTTCACCACATAGTTTTA 1021
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Db       1012 TGGGAGAGAGAAGGAAGGATGCCTTGGGAGTGCTTGAGTA-GCTTCTCAAGTGTCTTTTC 1070

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RESULT 9
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LOCUS BM924942 1063 bp mRNA linear EST 12-MAR-2002
DEFINITION AGENCOURT_6627575 NIH_MGC_122 Homo sapiens cDNA clone IMAGE:5762204 5', mRNA sequence.
ACCESSION BM924942
VERSION BM924942.1 GI:19375321
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 1063)
AUTHORS NIH-MGC http://mgc.nci.nih.gov/.
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Life Technologies, Inc.
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLAM12812 row: a column: 21
High quality sequence stop: 714.
FEATURES Location/Qualifiers
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/note="Organ: pooled lung and spleen; Vector: pCMV-SPORT6; Site_1: NotI; Site_2: EcoRV (destroyed); RNA source anonymous pool of 24 week female lung, 16 week female spleen, and 20-22 week male spleens. Library is oligo-dT primed and directionally cloned (EcoRV site is destroyed upon cloning). Average insert size 1.4 kb, insert size range 1-3 kb. Library is normalized and enriched for full-length clones and was constructed by C. Gruber (Invitrogen). Research Genetics tracking code 026. Note: this is a NIH_MGC Library."
ORIGIN

Query Match 51.7%; Score 893.8; DB 12; Length 1063;
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Matches 1014; Conservative 0; Mismatches 27; Indels 14; Gaps 9;

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Qy        855 TT--CTTGTTAACGTAATAATAGAGACA-TTTTTAAAAGCACACAGCTCAAAGTCAGCCA 911
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Qy        912 ATAAGTC--TTTTCCTATTTGTGAC-TTTTACTAATAAAAATAAATCTGCC--TGTAAAT 966
Db        909 ATAAAGCCTTTTCCCTATTTGTGACTTTTTACTAATAAAAATAAATCTGCCCTGTAAAAT 968

Qy        967 TATCTTGAAGT-CCTTTACCTGGAACAAGCACTCTC---TTTTTCACCACATAGTTTTAA 1022
Db        969 TATCTTGAAGTCCCTTTACCTGGAAACAACACTCTCCTTTTTTCACCCATAGGTTTTAAA 1028

Qy       1023 CTTGACTTTCAAGATAATTTTCAGGGTTTTTGTTG 1057
Db       1029 CTTGACTTTCAAAAAAATTTTCGGGTTTTTTGTTG 1063
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RESULT 10
AL567498/c
LOCUS AL567498 962 bp mRNA linear EST 31-MAY-2003
DEFINITION AL567498 Homo sapiens FETAL BRAIN Homo sapiens cDNA clone CS0DF037YD23 3-PRIME, mRNA sequence.
ACCESSION AL567498
VERSION AL567498.2 GI:31290393
KEYWORDS EST.

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SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 962)
  AUTHORS   Li,W.B., Gruber,C., Jessee,J. and Polayes,D.
  TITLE     Full-length cDNA libraries and normalization
  JOURNAL   Unpublished (2001)
COMMENT     On Feb 16, 2001 this sequence version replaced gi:12920917.
            Contact: Genoscope
            Genoscope - Centre National de Sequencage
            BP 191 91006 EVRY cedex - France
            Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr
            Library was constructed by Life Technologies, a division of
            Invitrogen. This sequence belongs to sequence cluster 6173.r,
            Contact : Feng Liang Email : fliang@lifetech.com URL :
            http://fulllength.invitrogen.com/ InVitroGen Corporation 1600
            Faraday Avenue Genoscope sequence ID : CS0DF037CB12NP1.
FEATURES             Location/Qualifiers
     source          1. .962
                     /organism="Homo sapiens"
                     /mol_type="mRNA"
                     /db_xref="taxon:9606"
                     /clone="CS0DF037YD23"
                     /tissue_type="FETAL BRAIN"
                     /dev_stage="fetal"
                     /clone_lib="Homo sapiens FETAL BRAIN"
                     /note="Organ: brain; Vector: pCMVSPORT_6; 1st strand cDNA
                     was primed with a NotI-oligo(dT) primer. Five prime end
                     enriched, double-strand cDNA was digested with Not I and
                     cloned into the Not I and EcoRV sites of the pCMVSPORT 6
                     vector. Library was not normalized."
ORIGIN
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  Query Match             51.7%;  Score 893.4;  DB 9;  Length 962;
  Best Local Similarity   93.8%;  Pred. No. 2.9e-159;
  Matches  903;  Conservative   40;  Mismatches   18;  Indels    2;  Gaps    2;

Qy        728 AAGAAACAGGCAGACAACTGGAAAGAACTGACTGGGTTTTGCTGGGTTTCATTTTAATAC 787
              ||:|||:|:|||||||||||:||:|||||  :|||||:|||||||:|||||||:|||||||
Db        962 AARAAAMAKGCAGACAACTGRAAWGAACTTWCTGGGKTTTGCTGKGTTTCATKTTAATAC 903

Qy        788 CTTGTTGATTTCA-CCAACTGTTGCTGGAAGATTCAAAACTGGAAGCAAAAACTTGCTTG 846
              |||||||||||||  ||:|||||||:|||||||||||||:||||:|||||||||||||||||
Db        902 CTTGTTGATTTCACCCWACTGTTGYTGGAAGATTCAAWACTGRAAGCAAAAACTTGCTTG 843

Qy        847 ATTTTTTTTTTCTTGTTAACGTAATAATAGAGACATTTTTAAAAGCACACAGCTCAAAGTC 906
              ||||||||||||||||||||||||:|||||||||||||||:|:||| |||||||||
Db        842 ATTTTTTTTTTCTTGTTAACGTAATAAWAGAGACATTTTTAAAAGYAYACATCTCAAAGTC 783

Qy        907 AGCCAATAAGTCTTTTCCTATTTGTGACTTTTACTAATAAAAATAAATCTGCCTGTAAAT 966
              |||||||||||||||||||||||||||||||||||||||||||||:|||||||||||||||
Db        782 AGCCAATAAGTCTTTTCCTATTTGTGACTTTTACTAATAAAAAWAAATCTGCCTGTAAAT 723

Qy        967 TATCTTGAAGTCCTTTACCTGGAACAAGCACTCTCTTTTTCACCACATAGTTTTAACTTG 1026
              |||||||||||||||||:|||||||||||||||||||:|||||||||||||||||||||||
Db        722 TATCTTGAAGTCCTTTWCCTGGAACAAGCACTCTCTBTTTCACCACATAGTTTTAACTAM 663

Qy       1027 ACTTTCAAGATAATTTTCAGGGTTTTTGTTGTTGTTGTTTTTTGTTTGTTTGTTTTGGTG 1086
              ||| |||||| ||| :||||:|||||||||||||||||||||||||||||||||||||||
Db        662 ACTCTCAAGAAAATAYTCAGSGTTTTTGTTGTTGTTGTTTTTTGTTTGTTTGTTTTGGTG 603

Qy       1087 GGAGAGGGGAGGGATGCCTGGGAAGTGGTTAACAACTTTTTTCAAGTCACTTTACTAAAC 1146
              |:|||||||||||||||||||||||||||||||||:|||||||||||||||| || ||||
Db        602 GRAGAGGGGAGGGATGCCTGGGAAGTGGTTAACAACKTTTTTCAAGTCACTTAACAAAAC 543

Qy       1147 AAACTTTTGTAAATAGACCTTACCTTCTATTTTCGAGTTTCATTTATATTTTGCAGTGTA 1206
              ||||:||||:|||:|||||||||||||||||||||||| ||||||||||||||||||||||
Db        542 AAACKTTTGWAAAWAGACCTTACCTTCTATTTTCGAGTCTCATTTATATTTTGCAGTGTA 483

Qy       1207 GCCAGCCTCATCAAAGAGCTGACTTACTCATTTGACTTTTGCACTGACTGTATTATCTGG 1266
              ||||||||||||||||||:|||||||||||||||||||||||||||||:||||||||||
Db        482 GCCAGCCTCATCAAAGAGCTVACTTACTCATTTGACTTTTGCACTGACTGWATTATCTGG 423
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Qy       1267 GTATCTGCTGTGTCTGCACTTCATGGTAAACGGGATCTAAAATGCCTGGTGGCTTTTCAC 1326
              |||||||||||||||||| ||||||||||||||||||||||||||||||||||||||||||
Db        422 GTATCTGCTGTGTCTGCACCTCATGGTAAACGGGATCTAAAATGCCTGGTGGCTTTTCAC 363

Qy       1327 AAAAAGCAGATTTTCTTCATGTACTGTGATGTCTGATGCAATGCATCCTAGAACAAACTG 1386
              ||||||||||::|| |||||||||||||:||:||:|||||||| ||||||||||||||||
Db        362 AAAAAGCAGATYYTCCTCATGTACTGTGATSTCYGAYGCAATGCACCCTAGAACAAACTG 303

Qy       1387 GCCATTTGCTAGTTTACTCTAAAGACTAAACATAGTCTTGGTGTGTGTGGTCTTACTCAT 1446
              ||||||||||||:|||||||||||||||||||||||||||||||||:||||||||||
Db        302 CCCATTTGCTAGTTYACTCTAAAGACTAAACATAGTCTTGGTGTGTGTGSTCTTACTCAT 243

Qy       1447 CTTCTAGTACCTTTAAGGACAAATCCTAAGGACTTGGACACTTGCAATAAAGAAATTTTA 1506
              |||||||||||||||||||||||||||||||||||||||||:||||||||||||||||||
Db        242 CTTCTAGTACCTTTAAGGACAAATCCTAAGGACTTGGACACTYGCAATAAAGAAATTTTA 183

Qy       1507 TTTTAAACCCAAGCCTCCCTGGATTGATAATATATACACATTTGTCAGCATTTCCGGTCG 1566
              |:|||||||||||||||||||||||||||||||||||||||||||||||||||||:||
Db        182 TYTTAAACCCAAGCCTCCCTGGATTGATAATATATACACATTTGTCAGCATTTCCGGYCG 123

Qy       1567 TGGTGAGAGGCAGCTGTTTGAGCTCCAATATGTGCAGCTTTGAACTAGGGCTGGGGTTGT 1626
              |||||||||||||||||||||||||| ||||| |||||||| |||||||||:||||||||
Db        122 TGGTGAGAGGCAGCTGTTTGAGCCCCAATGTGTGCAGCCTTGAACTAGSGCTGGGGTTGT 63

Qy       1627 GGGTGCCTCTTCTGAAAGGTCTAACCATTATTGGATAACTGGCTTTTTTCTTCCTATGTC 1686
              ||||||: |||||||||||||||||||||||||||||| ||||||||||||||||||||
Db          62 GGGTGCMCCTTCTGAAAGGTCTAACCATTATTGGATAACT-GCTTTTTTCTTCCTATGTC 4

Qy       1687 CTC 1689
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Db           3 CTC 1
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RESULT 11
BX439642
LOCUS       BX439642                1201 bp    mRNA    linear   EST 15-MAY-2003
DEFINITION  BX439642 Homo sapiens PLACENTA Homo sapiens cDNA clone CS0DE012YN20
            5-PRIME, mRNA sequence.
ACCESSION   BX439642
VERSION     BX439642.1  GI:30789776
KEYWORDS    EST.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 1201)
  AUTHORS   Li,W.B., Gruber,C., Jessee,J. and Polayes,D.
  TITLE     Full-length cDNA libraries and normalization
  JOURNAL   Unpublished (2001)
COMMENT     Contact: Genoscope
            Genoscope - Centre National de Sequencage
            BP 191 91006 EVRY cedex - France
            Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr
            Library was constructed by Life Technologies, a division of
            Invitrogen. This sequence belongs to sequence cluster 6173.r
            Contact : Feng Liang Email : fliang@lifetech.com URL :
            http://fulllength.invitrogen.com/ InVitroGen Corporation 1600
            Faraday Avenue Genoscope sequence ID : CS0DE012DG10QP1.
FEATURES             Location/Qualifiers
     source          1. .1201
                     /organism="Homo sapiens"
                     /mol_type="mRNA"
                     /db_xref="taxon:9606"
                     /clone="CS0DE012YN20"
                     /tissue_type="PLACENTA"
                     /clone_lib="Homo sapiens PLACENTA"
                     /note="Vector: pCMVSPORT_6; 1st strand cDNA was primed
                     with a NotI-oligo(dT) primer. Five prime end enriched,
                     double-strand cDNA was digested with Not I and cloned into
                     the Not I and EcoRV sites of the pCMVSPORT 6 vector.
                     Library was not normalized."
ORIGIN
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  Query Match             51.6%;  Score 891.4;  DB 13;  Length 1201;
  Best Local Similarity   99.2%;  Pred. No. 6.7e-159;
  Matches  914;  Conservative    2;  Mismatches    3;  Indels    2;  Gaps    2;

Qy        207 AGAATTTCGAGGATGTCAGATGTAAATGTATCTGCCCTCCCTATAAAGAAAATTCTGGGC 266
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        105 AGAATTTCGAGGATGTCAGATGTAAATGTATCTGCCCTCCCTATAAAGAAAATTCTGGGC 164

Qy        267 ATATTTATAATAAGAACATATCTCAGAAAGATTGTGATTGCCTTCATGTTGTGGAGCCCA 326
              |||||||||||||||||||||||||||||||||||||||||||||||||| ||||||||||
Db        165 ATATTTATAATAAGAACATATCTCAGAAAGATTGTGATTGCCTTCATGTCGTGGAGCCCA 224

Qy        327 TGCCTGTGCGGGGGCCTGATGTAGAAGCATACTGTCTACGCTGTGAATGCAAATATGAAG 386
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        225 TGCCTGTGCGGGGGCCTGATGTAGAAGCATACTGTCTACGCTGTGAATGCAAATATGAAG 284

Qy        387 AAAGAAGCTCTGTCACAATCAAGGTTACCATTATAATTTATCTCTCCATTTTGGGCCTTC 446
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        285 AAAGAAGCTCTGTCACAATCAAGGTTACCATTATAATTTATCTCTCCATTTTGGGCCTTC 344

Qy        447 TACTTCTGTACATGGTATATCTTACTCTGGTTGAGCCCATACTGAAGAGGCGCCTCTTTG 506
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        345 TACTTCTGTACATGGTATATCTTACTCTGGTTGAGCCCATACTGAAGAGGCGCCTCTTTG 404

Qy        507 GACATGCACAGTTGATACAGAGTGATGATGATATTGGGGATCACCAGCCTTTTGCAAATG 566
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        405 GACATGCACAGTTGATACAGAGTGATGATGATATTGGGGATCACCAGCCTTTTGCAAATG 464

Qy        567 CACACGATGTGCTAGCCCGCTCCCGCAGTCGAGCCAACGTGCTGAACAAGGTAGAATATG 626
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        465 CACACGATGTGCTAGCCCGCTCCCGCAGTCGAGCCAACGTGCTGAACAAGGTAGAATATG 524

Qy        627 CACAGCAGCGCTGGAAGCTTCAAGTCCAAGAGCAGCGAAAGTCTGTCTTTGACCGGCATG 686
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        525 CACAGCAGCGCTGGAAGCTTCAAGTCCAAGAGCAGCGAAAGTCTGTCTTTGACCGGCATG 584

Qy        687 TTGTCCTCAGCTAATTGGGAATTGAATTCAAGGTGACTAGAAAGAAACAGGCAGACAACT 746
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        585 TTGTCCTCAGCTAATTGGGAATTGAATTCAAGGTGACTAGAAAGAAACAGGCAGACAACT 644

Qy        747 GGAAAGAACTGACTGGGTTTTGCTGGGTTTCATTTTAATACCTTGTTGATTTCACCAACT 806
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        645 GGAAAGAACTGACTGGGTTTTGCTGGGTTTCATTTTAATACCTTGTTGATTTCACCAACT 704

Qy        807 GTTGCTGGAAGATTCAAAACTGGAAGCAAAAACTTGCTTGATTTTTTTTTCTTGTTAACG 866
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        705 GTTGCTGGAAGATTCAAAACTGGAAGCAAAAACTTGCTTGATTTTTTTTTCTTGTTAACG 764

Qy        867 TAATAATAGAGACATTTTTAAAAGCACACAGCTCAAAGTCAGCCAATAAGTCTTTTCCTA 926
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        765 TAATAATAGAGACATTTTTAAAAGCACACAGCTCAAAGTCAGCCAATAAGTCTTTTCCTA 824

Qy        927 TTTGTGACTTTTACTAATAAAAATAAATCTGCCTGTAAATTATCTTGAAGTCCTTTACCT 986
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        825 TTTGTGACTTTTACTAATAAAAATAAATCTGCCTGTAAATTATCTTGAAGTCCTTTACCT 884

Qy        987 GGAACAAGCACTCTCTTTTTCACCACATAGTTTTAACTTGACTTTCAAGATAATTTTCAG 1046
              |||||||||||||||||||||||||||||||||||||||||||||||| ||||||||||||
Db        885 GGAACAAGCACTCTCTTTTTCACCACATAGTTTTAACTTGACCTTCAAGATAATTTTCAG 944

Qy       1047 GGTTTTTGTTGTTGTTGTTTTTTGTTTGTTTGTTTTGGTGGGAGAGGGGAGGGATGCCTG 1106
              |||||||||||||||| |||||||||||||||||||||||||||||||||||||| |||
Db        945 GGTTTTTGTTGTTGTTG-TTTTTGTTTGTTTGTTTTGGTGGGAGAGGGGAGGGATG-CTG 1002

Qy       1107 GGAAGTGGTTAACAACTTTTT 1127
              |||||||||||:|: |||||
Db       1003 GGAAGTGGTTAAMAMTTTTTT 1023


RESULT 12
AL552487
LOCUS       AL552487               1201 bp    mRNA    linear   EST 31-MAY-2003
DEFINITION  AL552487 Homo sapiens PLACENTA COT 25-NORMALIZED Homo sapiens cDNA
            clone CS0DI070YH13 5-PRIME, mRNA sequence.
ACCESSION   AL552487
VERSION     AL552487.2  GI:31274302
KEYWORDS    EST.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 1201)
  AUTHORS   Li,W.B., Gruber,C., Jessee,J. and Polayes,D.
  TITLE     Full-length cDNA libraries and normalization
  JOURNAL   Unpublished (2001)
COMMENT     On Feb 15, 2001 this sequence version replaced gi:12891431.
            Contact: Genoscope
            Genoscope - Centre National de Sequencage
            BP 191 91006 EVRY cedex - France
            Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr
            Library was constructed by Life Technologies, a division of
            Invitrogen. This sequence belongs to sequence cluster 6242.f For
            more information about this cluster, see
            http://www.genoscope.cns.fr/
            cgi-bin/cluster.cgi?seq=CS0DI070CD07QP1&cluster=6242.f. Contact :
            Feng Liang Email : fliang@lifetech.com URL :
            http://fulllength.invitrogen.com/ InVitroGen Corporation 1600
            Faraday Avenue Genoscope sequence ID : CS0DI070CD07QP1.
FEATURES             Location/Qualifiers
     source          1. .1201
                     /organism="Homo sapiens"
                     /mol_type="mRNA"
                     /db_xref="taxon:9606"
                     /clone="CS0DI070YH13"
                     /tissue_type="PLACENTA COT 25-NORMALIZED"
                     /clone_lib="Homo sapiens PLACENTA COT 25-NORMALIZED"
                     /note="1st strand cDNA was primed with a NotI-oligo(dT)
                     primer. Five prime end enriched, double-strand cDNA was
                     digested with Not I and cloned into the Not I and EcoR V
                     sites of the pCMVSPORT 6 vector. Library was normalized."
ORIGIN

  Query Match             51.6%;  Score 890.8;  DB 9;  Length 1201;
  Best Local Similarity   98.5%;  Pred. No. 8.7e-159;
  Matches  936;  Conservative    4;  Mismatches    6;  Indels    4;  Gaps    4;

Qy          1 CAGCCGGGTCCCAAGCCTGTGCCTGAGCCTGAGCCTGAGCCTGAGCCCGAGCCGGGAGCC 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         82 CAGCCGGGTCCCAAGCCTGTGCCTGAGCCTGAGCCTGAGCCTGAGCCCGAGCCGGGAGCC 141

Qy         61 GGTCGCGGGGGGCTCCGGGCTGTGGGACCGCTGGGCCCCCAGCGATGGCGACCCTGTGGGG 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        142 GGTCGCGGGGGGCTCCGGGCTGTGGGACCGCTGGGCCCCCAGCGATGGCGACCCTGTGGGG 201

Qy        121 AGGCCTTCTTCGGCTTGGCTCCTTGCTCAGCCTGTCGTGCCTGGCGCTTTCCGTGCTGCT 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        202 AGGCCTTCTTCGGCTTGGCTCCTTGCTCAGCCTGTCGTGCCTGGCGCTTTCCGTGCTGCT 261

Qy        181 GCTGGCGCAGCTGTCAGACGCCGCCAAGAATTTCGAGGATGTCAGATGTAAATGTATCTG 240
              |||||||| |||||||||||||||||||||||||||||||||||||||||||||||||||
Db        262 GCTGGCGCA-CTGTCAGACGCCGCCAAGAATTTCGAGGATGTCAGATGTAAATGTATCTG 320

Qy        241 CCCTCCCTATAAAGAAAATTCTGGGCATATTTATAATAAGAACATATCTCAGAAAGATTG 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        321 CCCTCCCTATAAAGAAAATTCTGGGCATATTTATAATAAGAACATATCTCAGAAAGATTG 380

Qy        301 TGATTGCCTTCATGTTGTGGAGCCCATGCCTGTGCGGGGGCCTGATGTAGAAGCATACTG 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        381 TGATTGCCTTCATGTTGTGGAGCCCATGCCTGTGCGGGGGCCTGATGTAGAAGCATACTG 440

Qy        361 TCTACGCTGTGAATGCAAATATGAAGAAAGAAGCTCTGTCACAATCAAGGTTACCATTAT 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        441 TCTACGCTGTGAATGCAAATATGAAGAAAGAAGCTCTGTCACAATCAAGGTTACCATTAT 500

Qy        421 AATTTATCTCTCCATTTTGGGCCTTCTACTTCTGTACATGGTATATCTTACTCTGGTTGA 480
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Db        501 AATTTATCTCTCCATTTTGGGCCTTCTACTTCTGTACATGGTATATCTTACTCTGGTTGA 560

Qy        481 GCCCATACTGAAGAGGCGCCTCTTTGGACATGCACAGTTGATACAGAGTGATGATGATAT 540

Db        561 GCCCATACTGAAGAGGCGCCTCTTTGGACATGCACAGTTGATACAGAGTGATGATGATAT 620

Qy        541 TGGGGATCACCAGCCTTTTGCAAATGCACACGATGTGCTAGCCCGCTCCCGCAGTCGAGC 600

Db        621 TGGGGATCACCAGCCTTTTGCAAATGCACACGATGTGCTAGCCCGCTCCCGCAGTCGAGC 680

Qy        601 CAACGTGCTGAACAAGGTAGAATATGCACAGCAGCGCTGGAAGCTTCAAGTCCAAGAGCA 660

Db        681 CAACGTGCTGAACAAGGTAGAATATGCACAGCAGCGCTGGAAGCTTCAAGTCCAAGAGCA 740

Qy        661 GCGAAAGTCTGTCTTTGACCGGCATGTTGTCCTCAGCTAATTGGGAATTGAATTCAAGGT 720

Db        741 GCGAAAGTCTGTCTTTGACCGGCATGTTGTCCTCAGCTAATTGGGAATTGAATTCAAGGT 800

Qy        721 GACTAGAAAGAAACAGGCAGACAACTGGAAAGAACTGACTGGGTTTTGCTGGGTTTCATT 780

Db        801 GACTAGAAAGAAACAGGCAGACAACTGGAAAGAACTGACTGGGTTTTGCTGGGTTTCATT 860

Qy        781 TTAATACCTTGTTGATTTCACCAACTGTTGCTGGAAGATTCAAAACTGGAAGCAAAAACT 840

Db        861 TTAATACCTTGTTGATTTCACCAACTGTTGCTGGAAGATTCAAAACTGGAAGCAAAAACT 920

Qy        841 TGCTTGATTTTTTTTTCTTGTTAACGTAATAATAGAGACATTTTTAAAAGCACACAGCTC 900

Db        921 TGCTTGATTTTTTTTTCTTGTTAACGTAATAATAGAGACATTTTTAAAA-SACACAGCTC 979

Qy        901 AAAGTCAGCCAATAAGTCTTTTCCTATTTGTGACTTTTACTAATAAAAAT 950

Db        980 -AARKCAGCCAATAAGTC-TTTCCTATTTGTGACTTTACTATAAAAWAAT 1027


RESULT 13
AL552032
LOCUS       AL552032               1190 bp    mRNA    linear   EST 31-MAY-2003
DEFINITION  AL552032 Homo sapiens PLACENTA COT 25-NORMALIZED Homo sapiens cDNA
            clone CS0DI060YL12 5-PRIME, mRNA sequence.
ACCESSION   AL552032
VERSION     AL552032.2  GI:31273848
KEYWORDS    EST.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 1190)
  AUTHORS   Li,W.B., Gruber,C., Jessee,J. and Polayes,D.
  TITLE     Full-length cDNA libraries and normalization
  JOURNAL   Unpublished (2001)
COMMENT     On Feb 15, 2001 this sequence version replaced gi:12890542.
            Contact: Genoscope
            Genoscope - Centre National de Sequencage
            BP 191 91006 EVRY cedex - France
            Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr
            Library was constructed by Life Technologies, a division of
            Invitrogen. This sequence belongs to sequence cluster 6242.f For
            more information about this cluster, see
            http://www.genoscope.cns.fr/
            cgi-bin/cluster.cgi?seq=CS0DI060DF06QP1&cluster=6242.f. Contact :
            Feng Liang Email : fliang@lifetech.com URL :
            http://fulllength.invitrogen.com/ InVitroGen Corporation 1600
            Faraday Avenue Genoscope sequence ID : CS0DI060DF06QP1.
FEATURES             Location/Qualifiers
     source          1. .1190
                     /organism="Homo sapiens"
                     /mol_type="mRNA"
                     /db_xref="taxon:9606"
                     /clone="CS0DI060YL12"
                     /tissue_type="PLACENTA COT 25-NORMALIZED"
                     /clone_lib="Homo sapiens PLACENTA COT 25-NORMALIZED"
                     /note="1st strand cDNA was primed with a NotI-oligo(dT)
                     primer. Five prime end enriched, double-strand cDNA was
                     digested with Not I and cloned into the Not I and EcoR V
                     sites of the pCMVSPORT 6 vector. Library was normalized."
ORIGIN

  Query Match             51.4%;  Score 888.6;  DB 9;  Length 1190;
  Best Local Similarity   89.7%;  Pred. No. 2.3e-158;
  Matches 1009;  Conservative   23;  Mismatches   72;  Indels   21;  Gaps    7;

Qy         17 CTGTGCCTGAGCCTGAGCCTGAGCCTGAGCCCGAGCCGGGAGCCGGTCGCGGGGGCTCCG 76

Db         54 CTGAGCCTGAGCCTGAGCCTGAGCCTGAGCCCGAGCCGGGAGCCGGTCGCGGGGGCTCCG 113

Qy         77 GGCTGTGGGACCGCTGGGCCCCCAGCGATGGCGACCCTGTGGGGAGGCCTTCTTCGGCTT 136

Db        114 GGCTGTGGGACCGCTGGGCCCCCAGCGATGGCGACCCTGTGGGGAGGCCTTCTTCGGCTT 173

Qy        137 GGCTCCTTGCTCAGCCTGTCGTGCCTGGCGCTTTCCGTGCTGCTGCTGGCGCAGCTGTCA 196

Db        174 GGCTCCTTGCTCAGCCTGTCGTGCCTGGCGCTTTCCGTGCTGCTGCTGGCGCA-STGTCA 232

Qy        197 GACGCCGCCAAGAATTTCGAGGATGTCAGATGTAAATGTATCTGCCCTCCCTATAAAGAA 256

Db        233 GACGCCGCCAAGAATTTCGAGGATGTCAGATGTAAATGTATCTGCCCTCCCTATAAAGAA 292

Qy        257 AATTCTGGGCATATTTATAATAAGAACATATCTCAGAAAGATTGTGATTGCCTTCATGTT 316

Db        293 AATTCTGGGCATATTTATAATAAGAACATATCTCAGAAAGATTGTGATTGCCTTCATGTC 352

Qy        317 GTGGAGCCCATGCCTGTGCGGGGGCCTGATGTAGAAGCATACTGTCTACGCTGTGAATGC 376

Db        353 GTGGAGCCCATGCCTGTGCGGGGGCCTGATGTAGAAGCATACTGTCTACGCTGTGAATGC 412

Qy        377 AAATATGAAGAAAGAAGCTCTGTCACAATCAAGGTTACCATTATAATTTATCTCTCCATT 436

Db        413 AAATATGAAGAAAGAAGCTCTGTCACAATCAAGGTTACCATTATAATTTATCTCTCCATT 472

Qy        437 TTGGGCCTTCTACTTCTGTACATGGTATATCTTACTCTGGTTGAGCCCATACTGAAGAGG 496

Db        473 TTGGGCCTTCTACTTCTGTACATGGTATATCTTACTCTGGTTGAGCCCATACTGAAGAGG 532

Qy        497 CGCCTCTTTGGACATGCACAGTTGATACAGAGTGATGATGATATTGGGGATCACCAGCCT 556

Db        533 CGCCTCTTTGGACATGCACAGTTGATACAGAGTGATGATGATATTGGGGATCACCAGCCT 592

Qy        557 TTTGCAAATGCACACGATGTGCTAGCCCGCTCCCGCAGTCGAGCCAACGTGCTGAACAAG 616

Db        593 TTTGCAAATGCACACGATGTGCTAGCCCGCTCCCGCAGTCGAGCCAACGTGCTGAACAAG 652

Qy        617 GTAGAATATGCACAGCAGCGCTGGAAGCTTCAAGTCCAAGAGCAGCGAAAGTCTGTCTTT 676

Db        653 GTAGAATATGCACAGCAGCGCTGGAAGCTTCAAGTCCAAGAGCAGCGAAAGTCTGTCTTT 712

Qy        677 GACCGGCATGTTGTCCTCAGCTAATTGGGAATTGAATTCAAGGTGACTAGAAAGAAACAG 736

Db        713 GACCGGCATGTTGTCCTCAGCTAATTGGGAATTGAATTCAAGGTGACTAGAAAGAAACAG 772

Qy        737 GCAGACAACTGGAAAGAACTGACTGGGTTTTGCTGGGTTTCATTTTAATACCTTGTTGAT 796

Db        773 GCAGACAACTGGAAAGAACTGACTGGGTTTTGCTGGGTTTCATTTTAATACCTTGTTGAT 832

Qy        797 TTCACCAACTGTTGCTGGAAGATTCAAAACTGGAAGCAAAAACTTGCTTGATTTTTTTTT 856

Db        833 TTCACCAACTGTTGCTGGAAGATTCAAAACTGGAAGCAAAAMCTTGCTTGATTTTTTTTT 892

Qy        857 CTTGTTAACGTAATAATAGAGACATTTTTAAAAGCACACAGCTCAAAGTCAGCCAATAAG 916

Db        893 CTTGTTAACGTAATAATAGAGACATTTTT-AAAGCACACAGCTCAAAGTCAGCCA--TAA 949

Qy        917 TCTTTTCCTATTTGTGACTTTTACTAATAAAAATAAATCTGCCTGTAAATTATCTTGAAG 976

Db        950 GTCTTTYCTATTTGTGACTTTACTAAWAAAAWAATCTGCTGTAAATAW------CTGGAA 1003
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Qy        977 TCCTTTACCTGGAACAAGCACTCTCTTTTTCACCACATAGTTTTAACTTGACTTTCAAGA 1036
              |:||||||||:||  |||| ||       |||| |   || :  ||||||||:
Db       1004 GTCYTTACCTGGAMCAGCCTCTCTTTT------CACACATAGTTTWACTGACTTTCAR-- 1055

Qy       1037 TAATTTTCAGGGTTTTTGTTGTTG--TTGTTTTTTGTTTGTTTGTTTTGGTGGGAGAGGG 1094
              |: |||||||:||| || ||:||  ||||| ::|||||||  |    || ||     |||
Db       1056 -AWATTTCAGGKTTTGTGGTGKTGTTTTGTTGKKTGTTTGTGGGGRAGGGGGGAGCTGGG 1114

Qy       1095 GAGGGATGCCTGGGAAGTGGTTAACAACTTTTTTCAAGTCACTTT 1139
              : ||    :|    |:|  ||:: ||  ||| | |:: | : ||
Db       1115 ARTGGTAAAMTTTTCARTMTTTMWAAAACTTTGTAAWRCCTMCTT 1159
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RESULT 14
AL576084/c
LOCUS AL576084 1201 bp mRNA linear EST 01-JUN-2003
DEFINITION AL576084 Homo sapiens PLACENTA COT 25-NORMALIZED Homo sapiens cDNA clone CS0DI071YI08 3-PRIME, mRNA sequence.
ACCESSION AL576084
VERSION AL576084.2 GI:31314380
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 1201)
AUTHORS Li,W.B., Gruber,C., Jessee,J. and Polayes,D.
TITLE Full-length cDNA libraries and normalization
JOURNAL Unpublished (2001)
COMMENT On Feb 16, 2001 this sequence version replaced gi:12937876.
Contact: Genoscope
Genoscope - Centre National de Sequencage
BP 191 91006 EVRY cedex - France
Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr
Library was constructed by Life Technologies, a division of Invitrogen. This sequence belongs to sequence cluster 6173.r
Contact : Feng Liang Email : fliang@lifetech.com URL : http://fulllength.invitrogen.com/ InVitroGen Corporation 1600 Faraday Avenue Genoscope sequence ID : CS0DI071BE04NP1.
FEATURES Location/Qualifiers
source 1. .1201
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="CS0DI071YI08"
/tissue_type="PLACENTA COT 25-NORMALIZED"
/clone_lib="Homo sapiens PLACENTA COT 25-NORMALIZED"
/note="1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime end enriched, double-strand cDNA was digested with Not I and cloned into the Not I and EcoR V sites of the pCMVSPORT 6 vector. Library was normalized."
ORIGIN

Query Match 51.2%; Score 884; DB 9; Length 1201;
Best Local Similarity 97.9%; Pred. No. 1.7e-157;
Matches 899; Conservative 4; Mismatches 14; Indels 1; Gaps 1;

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Qy        762 GGTTTTGCTGGGTTTCATTTTAATACCTTGTTGATTTCACCAACTGTTGCTGGAAGATTC 821
              || ||||  :|| |||||||||||||||| |:|||||||||||||||||||||||||||
Db        928 GGGTTTGGCKGGGTTCATTTTAATACCTTG-TKATTTCACCAACTGTTGCTGGAAGATTC 870

Qy        822 AAAACTGGAAGCAAAAACTTGCTTGATTTTTTTTTCTTGTTAACGTAATAATAGAGACAT 881
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        869 AAAACTGGAAGCAAAAACTTGCTTGATTTTTTTTTCTTGTTAACGTAATAATAGAGACAT 810

Qy        882 TTTTAAAAGCACACAGCTCAAAGTCAGCCAATAAGTCTTTTCCTATTTGTGACTTTTACT 941
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        809 TTTTAAAAGCACACAGCTCAAAGTCAGCCAATAAGTCTTTTCCTATTTGTGACTTTTACT 750

Qy        942 AATAAAAATAAATCTGCCTGTAAATTATCTTGAAGTCCTTTACCTGGAACAAGCACTCTC 1001
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        749 AATAAAAATAAATCTGCCTGTAAATTATCTTGAAGTCCTTTACCTGGAACAAGCACTCTC 690
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Qy       1002 TTTTTCACCACATAGTTTTAACTTGACTTTCAAGATAATTTTCAGGGTTTTTGTTGTTGT 1061
              ||||||||||||||||||||||||||:||||||||||||||||||||||||||||||||
Db        689 TTTTTCACCACATAGTTTTAACTTDACTTTCAAGATAATTTTCAGGGTTTTTGTTGTTGT 630

Qy       1062 TGTTTTTTGTTTGTTTGTTTTGGTGGGAGAGGGGAGGGATGCCTGGGAAGTGGTTAACAA 1121
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        629 TGTTTTTTGTTTGTTTGTTTTGGTGGGAGAGGGGAGGGATGCCTGGGAAGTGGTTAACAA 570

Qy       1122 CTTTTTTCAAGTCACTTTACTAAACAAACTTTTGTAAATAGACCTTACCTTCTATTTTCG 1181
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        569 CTTTTTTCAAGTCACTTTACTAAACAAACTTTTGTAAATAGACCTTACCTTCTATTTTCG 510

Qy       1182 AGTTTCATTTATATTTTGCAGTGTAGCCAGCCTCATCAAAGAGCTGACTTACTCATTTGA 1241
              |||||||||||||||||||||||||||||||||||||||||||||| ||| ||||||||||
Db        509 AGTTTCATTTATATTTTGCAGTGTAGCCAGCCTCATCAAAGAGCTAACTNACTCATTTGA 450

Qy       1242 CTTTTGCACTGACTGTATTATCTGGGTATCTGCTGTGTCTGCACTTCATGGTAAACGGGA 1301
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        449 CTTTTGCACTGACTGTATTATCTGGGTATCTGCTGTGTCTGCACTTCATGGTAAACGGGA 390

Qy       1302 TCTAAAATGCCTGGTGGCTTTTCACAAAAAGCAGATTTTCTTCATGTACTGTGATGTCTG 1361
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        389 TCTAAAATGCCTGGTGGCTTTTCACAAAAAGCAGATTTTCTTCATGTACTGTGATGTCTG 330

Qy       1362 ATGCAATGCATCCTAGAACAAACTGGCCATTTGCTAGTTTACTCTAAAGACTAAACATAG 1421
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        329 ATGCAATGCATCCTAGAACAAACTGGCCATTTGCTAGTTTACTCTAAAGACTAAACATAG 270

Qy       1422 TCTTGGTGTGTGTGGTCTTACTCATCTTCTAGTACCTTTAAGGACAAATCCTAAGGACTT 1481
              ||||||||||||||||||| ||||||||||||||||||||||||||||||||||||||||
Db        269 TCTTGGTGTGTGTGGTCTNACTCATCTTCTAGTACCTTTAAGGACAAATCCTAAGGACTT 210

Qy       1482 GGACACTTGCAATAAAGAAATTTTATTTTAAACCCAAGCCTCCCTGGATTGATAATATAT 1541
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        209 GGACACTTGCAATAAAGAAATTTTATTTTAAACCCAAGCCTCCCTGGATTGATAATATAT 150

Qy       1542 ACACATTTGTCAGCATTTCCGGTCGTGGTGAGAGGCAGCTGTTTGAGCTCCAATATGTGC 1601
              |||||||| |||||||||||||||||||||||||||||||||||||||||||||| :| ||
Db        149 ACACATTTNTCAGCATTTCCGGTCGTGGTGAGAGGCAGCTGTTTGAGCTCCAATGKGGGC 90

Qy       1602 AGCTTTGAACTAGGGCTGGGGTTGTGGGTGCCTCTTCTGAAAGGTCTAACCATTATTGGA 1661
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          89 AGCTTTGAACTAGGGCTGGGGTTGTGGGTGCCTCTTCTGAAAGGTCTAACCATTATTGGA 30

Qy       1662 TAACTGGCTTTTTTCTTC 1679
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Db          29 TNACTGGCTTTTTCTTCC 12
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RESULT 15
AL540345
LOCUS AL540345 953 bp mRNA linear EST 12-MAY-2003
DEFINITION AL540345 Homo sapiens PLACENTA Homo sapiens cDNA clone CS0DE001YO17 5-PRIME, mRNA sequence.
ACCESSION AL540345
VERSION AL540345.2 GI:30543405
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 953)
AUTHORS Li,W.B., Gruber,C., Jessee,J. and Polayes,D.
TITLE Full-length cDNA libraries and normalization
JOURNAL Unpublished (2001)
COMMENT On Feb 15, 2001 this sequence version replaced gi:12870404.
Contact: Genoscope
Genoscope - Centre National de Sequencage
BP 191 91006 EVRY cedex - France
Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr
Library was constructed by Life Technologies, a division of Invitrogen. This sequence belongs to sequence cluster 6173.r

```
            Contact : Feng Liang Email : fliang@lifetech.com URL :
            http://fulllength.invitrogen.com/ InVitroGen Corporation 1600
            Faraday Avenue Genoscope sequence ID : CS0DE001AH09QP1.
FEATURES              Location/Qualifiers
     source           1. .953
                      /organism="Homo sapiens"
                      /mol_type="mRNA"
                      /db_xref="taxon:9606"
                      /clone="CS0DE001YO17"
                      /tissue_type="PLACENTA"
                      /clone_lib="Homo sapiens PLACENTA"
                      /note="Vector: pCMVSPORT_6; 1st strand cDNA was primed
                      with a NotI-oligo(dT) primer. Five prime end enriched,
                      double-strand cDNA was digested with Not I and cloned into
                      the Not I and EcoRV sites of the pCMVSPORT 6 vector.
                      Library was not normalized."
ORIGIN

  Query Match             50.3%;  Score 869.2;  DB 9;  Length 953;
  Best Local Similarity   98.5%;  Pred. No. 1.1e-154;
  Matches  877;  Conservative    8;  Mismatches    4;  Indels    1;  Gaps    1;

Qy          5 CGGGTCCCAAGCCTGTGCCTGAGCCTGAGCCTGAGCCTGAGCCCGAGCCGGGAGCCGGTC 64
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         65 CGGGTCCCAAGCCTGTGCCTGAGCCTGAGCCTGAGCCTGAGCCCGAGCCGGGAGCCGGTC 124

Qy         65 GCGGGGGCTCCGGGCTGTGGGACCGCTGGGCCCCCAGCGATGGCGACCCTGTGGGGAGGC 124
              |||||||||||||||||||||||||||||||||||||||||||||:|||||||||||||
Db        125 GCGGGGGCTCCGGGCTGTGGGACCGCTGGGCCCCCAGCGATGGCGACCMTGTGGGGAGGC 184

Qy        125 CTTCTTCGGCTTGGCTCCTTGCTCAGCCTGTCGTGCCTGGCGCTTTCCGTGCTGCTGCTG 184
              :||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        185 MTTCTTCGGCTTGGCTCCTTGCTCAGCCTGTCGTGCCTGGCGCTTTCCGTGCTGCTGCTG 244

Qy        185 GCGCAGCTGTCAGACGCCGCCAAGAATTTCGAGGATGTCAGATGTAAATGTATCTGCCCT 244
              |||||| |||||||||||||||||||||||||||||||||||||||||||||||||:||
Db        245 GCGCAG-TGTCAGACGCCGCCAAGAATTTCGAGGATGTCAGATGTAAATGTATCTGCMCT 303

Qy        245 CCCTATAAAGAAAATTCTGGGCATATTTATAATAAGAACATATCTCAGAAAGATTGTGAT 304
              |: ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        304 CYWTATAAAGAAAATTCTGGGCATATTTATAATAAGAACATATCTCAGAAAGATTGTGAT 363

Qy        305 TGCCTTCATGTTGTGGAGCCCATGCCTGTGCGGGGGCCTGATGTAGAAGCATACTGTCTA 364
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Db        364 TGCHTTCATGTTGTGGAGCCCATGCCTGTGCGGGGGCCTGATGTAGAAGCATACTGTYTA 423

Qy        365 CGCTGTGAATGCAAATATGAAGAAAGAAGCTCTGTCACAATCAAGGTTACCATTATAATT 424
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Db        424 CGCTGTGAATGCAAATATGAAGAAAGAAGCTCTGTYACAATCAAGGTTACCATTATAATT 483

Qy        425 TATCTCTCCATTTTGGGCCTTCTACTTCTGTACATGGTATATCTTACTCTGGTTGAGCCC 484
              |||||||||||||||||||| ||||||||||||||||||||||||||||||||||||||
Db        484 TATCTCTCCATTTTGGGCCTTWTACTTCTGTACATGGTATATCTTACTCTGGTTGAGCCC 543

Qy        485 ATACTGAAGAGGCGCCTCTTTGGACATGCACAGTTGATACAGAGTGATGATGATATTGGG 544
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        544 ATACTGAAGAGGCGCCTCTTTGGACATGCACAGTTGATACAGAGTGATGATGATATTGGG 603

Qy        545 GATCACCAGCCTTTTGCAAATGCACACGATGTGCTAGCCCGCTCCCGCAGTCGAGCCAAC 604
              |||||||||||||||||||||| | ||||||||||||||||||||||||||||||||||
Db        604 GATCACCAGCCTTTTGCAAATGCANANGATGTGCTAGCCCGCTCCCGCAGTCGAGCCAAC 663

Qy        605 GTGCTGAACAAGGTAGAATATGCACAGCAGCGCTGGAAGCTTCAAGTCCAAGAGCAGCGA 664
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Db        664 GTGCTGAACAAGGTAGAATATGCACAGCAGCGCTGGAAGCTTCAAGTCCAAGAGCAGCGA 723

Qy        665 AAGTCTGTCTTTGACCGGCATGTTGTCCTCAGCTAATTGGGAATTGAATTCAAGGTGACT 724
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Db        724 AAGTCTGTCTTTGACCGGCATGTTGTCCTCAGCTAATTGGGAATTGAATTCAAGGTGACT 783

Qy        725 AGAAAGAAACAGGCAGACAACTGGAAAGAACTGACTGGGTTTTGCTGGGTTTCATTTTAA 784
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Db        784 AGAAAGAAACAGGCAGACAACTGGAAAGAACTGACTGGGTTTTGCTGGGTTTCATTTTAA 843

Qy        785 TACCTTGTTGATTTCACCAACTGTTGCTGGAAGATTCAAAACTGGAAGCAAAAACTTGCT 844
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||:|
Db        844 TACCTTGTTGATTTCACCAACTGTTGCTGGAAGATTCAAAACTGGAAGCAAAAACTTGYT 903

Qy        845 TGATTTTTTTTTCTTGTTAACGTAATAATAGAGACATTTTTAAAAGCACA 894
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Db        904 TGATTTTTTTTTCTTGTTAACGTAATAATAGAGACATTTTTAAAAGCACA 953

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Job time : 4587 secs
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